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OM protein - protein search, using sw model

Run on: June 21, 2004, 13:59:37 ; Search time 48 Seconds
(without alignments)
1952.669 Million cell updates/sec

Title: US-10-091-841A-9

Perfect score: 1706

Sequence: 1 MEGSAAPLRVCIIGSGP.....ALDAEHVLOEVGAQVGKSDZ 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1706	100.0	332	14	US-10-091-841-9
2	1702	99.8	331	14	Sequence 9, Appl
3	1581	92.7	333	12	Sequence 10, Appl
4	1581	92.7	333	12	Sequence 42556, A
5	1523	89.3	331	14	Sequence 58732, A
6	1469	86.1	310	14	Sequence 11, Appl
7	1346.5	78.9	383	12	Sequence 27, Appl
8	1346.5	78.9	383	12	Sequence 72, Appl
9	1346.5	78.9	383	14	Sequence 196, Appl
10	1334.5	78.2	383	12	Sequence 105, Appl
11	1334.5	78.2	383	12	Sequence 141, Appl
12	1334.5	78.2	383	14	Sequence 105, Appl
13	1334.5	78.2	383	14	Sequence 150, Appl
14	1333.5	78.2	383	12	Sequence 141, Appl
15	1333.5	78.2	383	14	Sequence 150, Appl

16	1332.5	78.1	383	12	US-10-290-072-87
17	1332.5	78.1	383	12	US-10-290-072-132
18	1332.5	78.1	383	14	US-10-141-531-87
19	1332.5	78.1	383	14	US-10-141-531-132
20	1330.5	78.0	383	12	US-10-290-072-186
21	1330.5	78.0	383	14	US-10-141-531-196
22	1326.5	77.8	383	12	US-10-290-072-114
23	1326.5	77.8	383	12	US-10-290-072-159
24	1326.5	77.8	383	12	US-10-290-072-177
25	1326.5	77.8	383	14	US-10-141-531-114
26	1326.5	77.8	383	14	US-10-141-531-159
27	1326.5	77.8	383	14	US-10-141-531-177
28	1325.5	77.7	383	12	US-10-290-072-96
29	1325.5	77.7	383	12	US-10-290-072-123
30	1325.5	77.7	383	12	US-10-290-072-195
31	1325.5	77.7	383	14	US-10-141-531-96
32	1325.5	77.7	383	14	US-10-141-531-123
33	1325.5	77.7	383	14	US-10-141-531-195
34	1324.5	77.6	383	12	US-10-290-072-168
35	1324.5	77.6	383	14	US-10-141-531-168
36	1324	77.6	333	9	US-09-897-898-3
37	1324	77.6	333	9	US-09-897-898-4
38	1324	77.6	333	9	US-09-897-898-14
39	1324	77.6	333	12	US-09-897-425-38
40	1324	77.6	333	12	US-09-897-425-39
41	1324	77.6	333	12	US-09-897-425-49
42	1324	77.6	333	14	US-10-032-201B-11
43	1324	77.6	333	14	US-10-032-201B-13
44	1324	77.6	333	14	US-10-032-201B-23
45	1324	77.6	365	12	US-10-290-072-61

ALIGNMENTS

RESULT 1
US-10-091-841-9
Sequence 9, Application US/10091841
Publication No. US20030150010A1
GENERAL INFORMATION:
APPLICANT: Cho, Myeong-Je
APPLICANT: Del Val, Greg
APPLICANT: Calliau, Maxime
APPLICANT: Lemauz, Peggy G.
APPLICANT: Buchanan, Bob B.
TITLE OF INVENTION: Barley Gene for Thioredoxin and
TITLE OF INVENTION: NADp-Thioredoxin Reductase
FILE REFERENCE: 2001-0701-30
CURRENT APPLICATION NUMBER: US/10/091,841
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: 09/540,014
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 60/127,198
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: US 60/169,162
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 60/177,740
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 60/177,739
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 332
TYPE: PRT
ORGANISM: Hordeum vulgare
US-10-091-841-9

Query Match 100.0%; Score 1706; DB 14; Length 332;
Best Local Similarity 100.0%; Pred. No. 3.8e-164;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEGSAAPLRVCIIGSGFAAHTAIYAARAEKPVLFEGWANDIAAGGQTTTTTVE 60

Db 1 MEGSAAAPLRTVCIIIGSGPAHTAAIYAARAEKLPVLEGGWANDIAAGGQTTTTTVE 60
QY 61 NFGPFTGIMGIDLMDCRAQSVRFCTNLSLSETVTEVDFSAFPFRVTSDSTTVLADTVV 120
Db 61 NFGPFTGIMGIDLMDCRAQSVRFCTNLSLSETVTEVDFSAFPFRVTSDSTTVLADTVV 120
QY 121 ATGAVARRLHFGSGDYNNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGNFLT KYG 180
Db 121 ATGAVARRLHFGSGDYNNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGNFLT KYG 180
QY 181 SQVYIIHRRNTFRASKIMQARALSNPKIQVWMDSEVVEAYGAGGGLAGVKVKNLVTGE 240
Db 181 SQVYIIHRRNTFRASKIMQARALSNPKIQVWMDSEVVEAYGAGGGLAGVKVKNLVTGE 240
QY 241 VSDLOVSGLFFAIGHEPATKFLNGQLEHADGVATKPGSTHTSVGVPFAAGDVQDKKYR 300
Db 241 VSDLOVSGLFFAIGHEPATKFLNGQLEHADGVATKPGSTHTSVGVPFAAGDVQDKKYR 300
QY 301 QAITAAGSGCMAALDAEHYLOEVGAQVGSZDZ 332
Db 301 QAITAAGSGCMAALDAEHYLOEVGAQVGSZDZ 332

RESULT 2

US-10-194-885-10
; Sequence 10, Application US/10194885
; Publication No. US20030135878A1
; GENERAL INFORMATION:

; APPLICANT: Wong, J. H.
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH ELEVATED
; FILE REFERENCE: THIOREDOXIN LEVELS
; CURRENT APPLICATION NUMBER: US/10/194,885
; PRIORITY FILING DATE: 2002-07-12
; PRIORITY FILING DATE: 2002-07-12
; PRIORITY FILING DATE: 2001-07-19
; PRIORITY FILING DATE: 2000-03-29
; PRIORITY FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Barley

US-10-194-885-10
Query Match 99.8%; Score 1702; DB 14; Length 331;
Best Local Similarity 100.0%; Pred. No. 9.5e-164;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGSAAAPLRTVCIIIGSGPAHTAAIYAARAEKLPVLEGGWANDIAAGGQTTTTTVE 60
Db 1 MEGSAAAPLRTVCIIIGSGPAHTAAIYAARAEKLPVLEGGWANDIAAGGQTTTTTVE 60
QY 61 NFGPFTGIMGIDLMDCRAQSVRFCTNLSLSETVTEVDFSAFPFRVTSDSTTVLADTVV 120
Db 61 NFGPFTGIMGIDLMDCRAQSVRFCTNLSLSETVTEVDFSAFPFRVTSDSTTVLADTVV 120
QY 121 ATGAVARRLHFGSGDYNNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGNFLT KYG 180
Db 121 ATGAVARRLHFGSGDYNNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGNFLT KYG 180
QY 181 SQVYIIHRRNTFRASKIMQARALSNPKIQVWMDSEVVEAYGAGGGLAGVKVKNLVTGE 240
Db 181 SQVYIIHRRNTFRASKIMQARALSNPKIQVWMDSEVVEAYGAGGGLAGVKVKNLVTGE 240
QY 241 VSDLOVSGLFFAIGHEPATKFLNGQLEHADGVATKPGSTHTSVGVPFAAGDVQDKKYR 300

Db 241 VSDLOVSGLFFAIGHEPATKFLNGQLEHADGVATKPGSTHTSVGVPFAAGDVQDKKYR 300
QY 301 QAITAAGSGCMAALDAEHYLOEVGAQVGSZDZ 331
Db 301 QAITAAGSGCMAALDAEHYLOEVGAQVGSZDZ 331

RESULT 3

US-10-425-114-42556
; Sequence 42556, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 42556
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700336177_FLI.pep
US-10-425-114-42556

Query Match 92.7%; Score 1581; DB 12; Length 333;
Best Local Similarity 91.8%; Pred. No. 1.8e-151;
Matches 304; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 MEGSAAAPLRTVCIIIGSGPAHTAAIYAARAEKLPVLEGGWANDIAAGGQTTTTTVE 60
Db 3 MEGSAAAPLRTVCIIIGSGPAHTAAIYAARAEKLPVLEGGWANDIAAGGQTTTTTVE 62
QY 61 NFGPFTGIMGIDLMDCRAQSVRFCTNLSLSETVTEVDFSAFPFRVTSDSTTVLADTVV 120
Db 63 NFGPFTGIMGIDLMDCRAQSVRFCTNLSLSETVTEVDFSAFPFRVTSDSTTVLADTVV 122
QY 121 ATGAVARRLHFGSGDYNNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGNFLT KYG 180
Db 123 ATGAVARRLHFGSGDYNNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGNFLT KYG 182
QY 181 SQVYIIHRRNTFRASKIMQARALSNPKIQVWMDSEVVEAYGAGGGLAGVKVKNLVTGE 240
Db 183 SHVYIIHRRNTFRASKIMQARALSNPKIQVWMDSEVVEAYGAGGGLAGVKVKNLVTGE 242
QY 241 VSDLOVSGLFFAIGHEPATKFLNGQLEHADGVATKPGSTHTSVGVPFAAGDVQDKKYR 300
Db 243 VSDLOVSGLFFAIGHEPATKFLNGQLEHADGVATKPGSTHTSVGVPFAAGDVQDKKYR 302
QY 301 QAITAAGSGCMAALDAEHYLOEVGAQVGSZDZ 331
Db 303 QAITAAGSGCMAALDAEHYLOEVGAQVGSZDZ 333

RESULT 4

US-10-425-114-58732
; Sequence 58732, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei

;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

;; FILE REFERENCE: 38-21(53313)B
;; CURRENT APPLICATION NUMBER: US/10/425,114

;; CURRENT FILING DATE: 2003-04-28

;; NUMBER OF SEQ ID NOS: 73128

;; SEQ ID NO 58732

;; LENGTH: 333

;; TYPE: PRT

;; ORGANISM: Zea mays

;; OTHER INFORMATION: Clone ID: 700447274_FLI.pcp

US-10-425-114-58732

Query Match 92.7%; Score 1581; DB 12; Length 333;
Best Local Similarity 91.8%; Pred. No. 1.8e-151;
Matches 304; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 MEGSAAPLRTRVCIIGSGPAHAHTAAIYAARAEKPVLFEGWMANDIAAGGQTTTTTIVE 60

DB 3 MEGSAAPLRTRVCIIGSGPAHAHTAAIYAARAEKPVLFEGWANDIAAGGQTTTTTIVE 62

QY 61 NFPGPTGIMGIDLMNCRAQSVFSGNLTSETVTEVDFSAARPRVTSSTVLADTVV 120

DB 63 NFPGPTGIMGADLMNCRAQSLRFGNLTSETVTAVDFAACPRVSADSTTVLADAVV 122

QY 121 ATGAVARLHFGSDTYWNRGISACVCDGAAPIFRNKPIAVIGGDSAMEEGNFLTXYG 180

DB 123 ATGAVARLHFGSDTYWNRGISACVCDGAAPIFRNKPIAVIGGDSAMEEGNFLTXYG 182

QY 181 SOVYIIHRRNTFRASKIMQARALSNPKIQVWVDSVVEAYGAGGGPLAGVKNLVTGE 240

DB 183 SHVYIIHRRNTFRASKIMQARALSNPKIKVLWDSVVEAYGAGGGPLAGVKNLANGE 242

QY 241 VSDLOVSGLFFAIGHEPATKFLNGQLHLDGYATKPGSTHTSVGVEAGDVQDKKYR 300

DB 243 VSDLOVSGLFFAIGHEPATKFLNGQLHLDGYATKPGSTHTSVGVEAGDVQDKKYR 302

QY 301 QAITAAGSGCMAALDAEHLQEVGAQVCKSD 331

DB 303 QAITAAGSGCMAALDAEHLQEVGAQVCKSD 333

RESULT 5

US-10-194-885-11

;; Sequence 11, Application US/10194885

;; Publication No. US20030135878A1

;; GENERAL INFORMATION:

;; APPLICANT: Wong, J. H.

;; APPLICANT: Cho, Myeong-Je

;; APPLICANT: Lemaux, Peggy G.

;; APPLICANT: Buchanan, Bob

;; TITLE OF INVENTION: TRANSGENIC PLANTS WITH ELEVATED

;; TITLE OF INVENTION: THIOREDUXIN LEVELS

;; FILE REFERENCE: 416272000800

;; CURRENT APPLICATION NUMBER: US/10/194,885

;; CURRENT FILING DATE: 2002-07-12

;; PRIOR APPLICATION NUMBER: 60/307,006

;; PRIOR FILING DATE: 2001-07-19

;; PRIOR APPLICATION NUMBER: 09/538,864

;; PRIOR FILING DATE: 2000-03-29

;; PRIOR APPLICATION NUMBER: 60/126,736

;; PRIOR FILING DATE: 1998-03-29

;; NUMBER OF SEQ ID NOS: 55

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 11

;; LENGTH: 331

;; TYPE: PRT

;; ORGANISM: wheat

US-10-194-885-11

Query Match 89.3%; Score 1523; DB 14; Length 331;

Best Local Similarity 87.9%; Pred. No. 1.3e-145;

Matches 291; Conservative 20; Mismatches 20; Indels 0; Gaps 0;

QY 1 MEGSAAPLRTRVCIIGSGPAHAHTAAIYAARAEKPVLFEGWMANDIAAGGQTTTTTIVE 60

DB 1 MEGSAAPLRTRVCIIGSGPAHAHTAAIYAARAEKPVLFEGWLANDIAAGGQTTTTTIVE 60

QY 61 NFPGPTGIMGIDLMNCRAQSVFSGNLTSETVTEVDFSAARPRVTSSTVLADTVV 120

DB 61 NFPGPTGILGIDLMNCRAQSVFSGNLTSETVTEVDFSAARPRVTSSTVLADTVV 120

QY 121 ATGAVARLHFGSDTYWNRGISACVCDGAAPIFRNKPIAVIGGDSAMEEGNFLTXYG 180

DB 121 ATGAVARLHFGSDTYWNRGISACVCDGAAPIFRNKPIAVIGGDSAMEEGNFLTXYG 180

QY 181 SOVYIIHRRNTFRASKIMQARALSNPKIQVWVDSVVEAYGAGGGPLAGVKNLVTGE 240

DB 181 SRVYIIHRRNTFRASKIMQARALSNPKIQVWVDSVVEAYGAGGGPLAGVKNLVTGE 240

QY 241 VSDLOVSGLFFAIGHEPATKFLNGQLHLDGYATKPGSTHTSVGVEAGDVQDKKYR 300

DB 241 VSDFRVAGLFFAIGHEPATKFLAGQLDSEGYATKPGSTHTSVKGVFAAGDVQDKKYR 300

QY 301 QAITAAGSGCMAALDAEHLQEVGAQVCKSD 331

DB 301 QAITAAGSGCMAALDAEHLQEVGAQVCKSD 331

RESULT 6

US-10-306-292-27

;; Sequence 27, Application US/10306292

;; Publication No. US20030145347A1

;; GENERAL INFORMATION:

;; APPLICANT: Lanahan, Michael B.

;; APPLICANT: Dessai, Nalini M.

;; APPLICANT: Gasdaska, Pamela Y.

;; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL

;; TITLE OF INVENTION: THEREIN

;; FILE REFERENCE: A-31383P1

;; CURRENT APPLICATION NUMBER: US/10/306,292

;; CURRENT FILING DATE: 2002-11-27

;; PRIOR APPLICATION NUMBER: US/09/598,747

;; PRIOR FILING DATE: 2000-06-21

;; NUMBER OF SEQ ID NOS: 42

;; SOFTWARE: PatentIn Ver. 2.1

;; SEQ ID NO 27

;; LENGTH: 310

;; TYPE: PRT

;; ORGANISM: Oryza sativa

US-10-306-292-27

Query Match 86.1%; Score 1469; DB 14; Length 310;

Best Local Similarity 91.6%; Pred. No. 3.6e-140;

Matches 283; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 1 MEGSAAPLRTRVCIIGSGPAHAHTAAIYAARAEKPVLFEGWMANDIAAGGQTTTTTIVE 60

DB 1 MEGSAAPLRTRVCIIGSGPAHAHTAAIYAARAEKPVLFEGWLANDIAAGGQTTTTTIVE 60

QY 61 NFPGPTGIMGIDLMNCRAQSVFSGNLTSETVTEVDFSAARPRVTSSTVLADTVV 120

DB 61 NFPGPTGILGIDLMNCRAQSVFSGNLTSETVTEVDFSAARPRVTSSTVLADTVV 120

QY 121 ATGAVARLHFGSDTYWNRGISACVCDGAAPIFRNKPIAVIGGDSAMEEGNFLTXYG 180

DB 121 ATGAVARLHFGSDTYWNRGISACVCDGAAPIFRNKPIAVIGGDSAMEEGNFLTXYG 180

QY 181 SOVYIIHRRNTFRASKIMQARALSNPKIQVWVDSVVEAYGAGGGPLAGVKNLVTGE 240

DB 181 SHVYIIHRRNTFRASKIMQARALSNPKIQVWVDSVVEAYGAGGGPLAGVKNLVTGE 240

QY 241 VSDLOVSGLFFAIGHEPATKFLNGQLHLDGYATKPGSTHTSVGVEAGDVQDKKYR 300

DB 241 ISDLQVSGLFFAIGHEPATKFLNGQLHLDGYATKPGSTHTSVKGVFAAGDVQDKKYR 300

QY 301 QAITAAGSG 309
 Db 301 QAITAAGSG 309

RESULT 7

US-10-290-072-72
 ; Sequence 72, Application US/10290072
 ; Publication No. US2003021151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Dalmia, Bipin K.
 ; APPLICANT: Desjarlais, John R.
 ; APPLICANT: Heifetz, Peter
 ; APPLICANT: Lugimbuhl, Peter
 ; APPLICANT: Muchhal, Umesh
 ; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
 ; FILE REFERENCE: A-71457-3
 ; CURRENT APPLICATION NUMBER: US/10/290,072
 ; CURRENT FILING DATE: 2002-11-06
 ; PRIOR APPLICATION NUMBER: US 60/370,609
 ; PRIOR FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: US 60/376,682
 ; PRIOR FILING DATE: 2002-04-29
 ; PRIOR APPLICATION NUMBER: US 10/141,531
 ; PRIOR FILING DATE: 2002-05-06
 ; PRIOR APPLICATION NUMBER: US 60/289,029
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 239
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 72
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-10-290-072-72

Query Match 78.9%; Score 1346.5; DB 12; Length 383;
 Best Local Similarity 76.8%; Pred. No. 1.3e-127;
 Matches 258; Conservative 39; Mismatches 31; Indels 9; Gaps 2;
 QY 4 SAAAPL-----RTRVCIIGSGPAAHTAAIYAARAELKPVLFEGWMANDIAAGGQLTITTD 58
 Db 47 SAAAVDMETHKTVCIVSGSPAAHTAAIYASRAELKPLLFEQWMANDIAPGGQLTITTD 106
 QY 59 VENPFGPTGIMGIDLMNCRASQVRFGNLSLSEVTEVDPSARPPRVTSSTTVLADTV 118
 Db 107 VENPFGPPEGILGIDIVEKFKQSERFGTTFITETVKNVDFSSKPKLFTDSRTVLADSV 166
 QY 119 VVATGAVARELHFGSGDT---YNNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGN 174
 Db 167 IISTGAVAKLSFTGSGEGNGGFWNRGISACAVCDGAAPIFRNKPLVIGGDSAMEEAN 226
 QY 175 FLTKYGSQVYIIHRRNTFRASKIMQARALSNPKIQVWDSVEVYAGGAGGPLAGVKVK 234
 Db 227 FLTKYGSQVYIIHRRDTFRASKIMQORALSNPKIEVWNSAVVEAYGDENGRVLGGLVKV 286
 QY 235 NLVTGEVSDIQVSGLFFAIGHEPATKFLNGQLEHLDADGVYATKPGSTHTSVSGVFAAGDV 294
 Db 287 NVVTGVDSDLVKVSGLFFAIGHEPATKFLDQLELDEDDGVYVTKPGTITKTSVGVFAAGDV 346
 QY 295 QDKKYRQAITAAGSGCMAALDAEHYLOEYGAQVKGSD 331
 Db 347 QDKKYRQAITAAGTGCMAALDAEHYLOEIGSQEGKSD 383

RESULT 8

US-10-141-531-72
 ; Sequence 72, Application US/10141531
 ; Publication No. US20030100743A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Briggs, Steven P.

APPLICANT: Dalmia, Bipin K.
 APPLICANT: del Val, Greg
 APPLICANT: Desjarlais, John R.
 APPLICANT: Heifetz, Peter
 APPLICANT: Lugimbuhl, Peter
 APPLICANT: Muchhal, Umesh
 TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
 FILE REFERENCE: A-71457-2/RET/BMS/RMK
 CURRENT APPLICATION NUMBER: US/10/141,531
 CURRENT FILING DATE: 2002-05-06
 PRIOR APPLICATION NUMBER: US 60/370,609
 PRIOR FILING DATE: 2002-04-05
 PRIOR APPLICATION NUMBER: US 60/289,029
 PRIOR FILING DATE: 2001-05-04
 NUMBER OF SEQ ID NOS: 208
 SOFTWARE: Patent in version 3.1
 SEQ ID NO 72
 LENGTH: 383
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 US-10-141-531-72

Query Match 78.9%; Score 1346.5; DB 14; Length 383;
 Best Local Similarity 76.6%; Pred. No. 1.3e-127;
 Matches 258; Conservative 39; Mismatches 31; Indels 9; Gaps 2;
 QY 4 SAAAPL-----RTRVCIIGSGPAAHTAAIYAARAELKPVLFEGWMANDIAAGGQLTITTD 58
 Db 47 SAAAVDMETHKTVCIVSGSPAAHTAAIYASRAELKPLLFEQWMANDIAPGGQLTITTD 106
 QY 59 VENPFGPTGIMGIDLMNCRASQVRFGNLSLSEVTEVDPSARPPRVTSSTTVLADTV 118
 Db 107 VENPFGPPEGILGIDIVEKFKQSERFGTTFITETVKNVDFSSKPKLFTDSRTVLADSV 166
 QY 119 VVATGAVARELHFGSGDT---YNNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGN 174
 Db 167 IISTGAVAKLSFTGSGEGNGGFWNRGISACAVCDGAAPIFRNKPLVIGGDSAMEEAN 226
 QY 175 FLTKYGSQVYIIHRRNTFRASKIMQARALSNPKIQVWDSVEVYAGGAGGPLAGVKVK 234
 Db 227 FLTKYGSQVYIIHRRDTFRASKIMQORALSNPKIEVWNSAVVEAYGDENGRVLGGLVKV 286
 QY 235 NLVTGEVSDIQVSGLFFAIGHEPATKFLNGQLEHLDADGVYATKPGSTHTSVSGVFAAGDV 294
 Db 287 NVVTGVDSDLVKVSGLFFAIGHEPATKFLDQLELDEDDGVYVTKPGTITKTSVGVFAAGDV 346
 QY 295 QDKKYRQAITAAGSGCMAALDAEHYLOEYGAQVKGSD 331
 Db 347 QDKKYRQAITAAGTGCMAALDAEHYLOEIGSQEGKSD 383

RESULT 9

US-10-032-201B-196
 ; Sequence 196, Application US/10032201B
 ; Publication No. US20030167524A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Rooijen, Gijb
 ; APPLICANT: Deckers, Harm
 ; APPLICANT: Heifetz, Peter Bernard
 ; APPLICANT: Briggs, Steven
 ; APPLICANT: Dalmia, Bipin Kumar
 ; APPLICANT: del Val, Greg
 ; APPLICANT: Moloney, Maurice
 ; APPLICANT: Zaplachinski, Steve
 ; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
 ; FILE REFERENCE: 38814 351B
 ; CURRENT APPLICATION NUMBER: US/10/032,201B
 ; CURRENT FILING DATE: 2001-12-19
 ; NUMBER OF SEQ ID NOS: 313
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 196
 ; LENGTH: 383

; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-032-201B-196

Query Match 78.9%; Score 1346.5; DB 14; Length 383;
Best Local Similarity 76.6%; Pred. No. 1.3e-127;
Matches 258; Conservative 39; Mismatches 31; Indels 9; Gaps 2;

QY 4 SAAAPL-----RTRVCIIGSGPAAHTAAIYAARAEKLPVLFEQWANDIAAGGQLTITTD 58
DB 47 SAAAVDMETHKTKVCIIVSGSPAHTAAIYASRAELKPLLFEGWANDIAAGGQLTITTD 106
QY 59 VENPFGPTGIMGIDLDNCRQAQSVRFGTNISETVTEVDFSAARPRVTSSTTVLADTV 118
DB 107 VENPFGPEGLIGDIVEKFKQSERFGTTFTETVKNVDFSSKPKLFTDSRTVLADSV 166
QY 119 VVATGAVARRLHFGSDT-----YNNRGISACAVCDGAAPFRNKPIAVIGGDSAMEEGN 174
DB 167 IISTGAVAKRLSFTSGGNGGFWNRGISACAVCDGAAPFRNKPLVVIIGGDSAMEEAN 226
QY 175 FLTKYGSQVYIHRNTFRASKIMQARALSNPKIOVWDSVVEAYGGAGGGLAGVKVK 234
DB 227 FLTKYGSKVIIHRTDFRASKIMQARALSNPKIEVWNSAVVEAYGNGRVLGGKVK 286
QY 235 NLVTGEVSDLVQSGLFFAIGHEPATKFLNGQLEHLDGYYVATKPGSTHTSVEGVFAAGDV 294
DB 287 NVVTGDSVSLKVSGLFFAIGHEPATKFLDQGLDEDEGYVTKPGTTKTSVGVFAAGDV 346
QY 295 QDKYRQAITAAGSCMAALDAEHYLOEVGAQVQKSD 331
DB 347 QDKYRQAITAAGTCMAALDAEHYLOEIGSQEGKSD 383

RESULT 10

US-10-290-072-105
; Sequence 105, Application US/10290072
; Publication No. US20030211511A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Daimia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Luginbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-3
; CURRENT APPLICATION NUMBER: US/10/290,072
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/376,682
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 105
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Arabidopsis thaliana variant
US-10-290-072-105

Query Match 78.2%; Score 1334.5; DB 12; Length 383;
Best Local Similarity 76.0%; Pred. No. 2.1e-126;
Matches 256; Conservative 39; Mismatches 33; Indels 9; Gaps 2;

QY 4 SAAAPL-----RTRVCIIGSGPAAHTAAIYAARAEKLPVLFEQWANDIAAGGQLTITTD 58
DB 47 SAAAVDMETHKTKVCIIVSGSPAHTAAIYASRAELKPLLFEGWANDIAAGGQLTITTD 106
QY 59 VENPFGPTGIMGIDLDNCRQAQSVRFGTNISETVTEVDFSAARPRVTSSTTVLADTV 118
DB 107 VENPFGPEGLIGDIVEKFKQSERFGTTFTETVKNVDFSSKPKLFTDSRTVLADSV 166
QY 119 VVATGAVARRLHFGSDT-----YNNRGISACAVCDGAAPFRNKPIAVIGGDSAMEEGN 174
DB 167 IISTGAVAKRLSFTSGGNGGFWNRGISACAVCDGAAPFRNKPLVVIIGGDSAMEEAN 226

DB 47 SAAAVDMETHKTKVCIIVSGSPAHTAAIYASRAELKPLLFEGWANDIAAGGQLTITTD 106
QY 59 VENPFGPTGIMGIDLDNCRQAQSVRFGTNISETVTEVDFSAARPRVTSSTTVLADTV 118
DB 107 VENPFGPEGLIGDIVEKFKQSERFGTTFTETVKNVDFSSKPKLFTDSRTVLADSV 166
QY 119 VVATGAVARRLHFGSDT-----YNNRGISACAVCDGAAPFRNKPIAVIGGDSAMEEGN 174
DB 167 IISTGAVAKRLSFTSGGNGGFWNRGISACAVCDGAAPFRNKPLVVIIGGDSAMEEAN 226
QY 175 FLTKYGSQVYIHRNTFRASKIMQARALSNPKIOVWDSVVEAYGGAGGGLAGVKVK 234
DB 227 FLTKYGSKVIIHRTDFRASKIMQARALSNPKIEVWNSAVVEAYGNGRVLGGKVK 286
QY 235 NLVTGEVSDLVQSGLFFAIGHEPATKFLNGQLEHLDGYYVATKPGSTHTSVEGVFAAGDV 294
DB 287 NVVTGDSVSLKVSGLFFAIGHEPATKFLDQGLDEDEGYVTKPGTTKTSVGVFAAGDV 346
QY 295 QDKYRQAITAAGSCMAALDAEHYLOEVGAQVQKSD 331
DB 347 QDKYRQAITAAGTCMAALDAEHYLOEIGSQEGKSD 383

RESULT 11

US-10-290-072-141
; Sequence 141, Application US/10290072
; Publication No. US20030211511A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Daimia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Luginbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-3
; CURRENT APPLICATION NUMBER: US/10/290,072
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/376,682
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 141
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Arabidopsis thaliana variant
US-10-290-072-141

Query Match 78.2%; Score 1334.5; DB 12; Length 383;
Best Local Similarity 76.0%; Pred. No. 2.1e-126;
Matches 256; Conservative 39; Mismatches 33; Indels 9; Gaps 2;

QY 4 SAAAPL-----RTRVCIIGSGPAAHTAAIYAARAEKLPVLFEQWANDIAAGGQLTITTD 58
DB 47 SAAAVDMETHKTKVCIIVSGSPAHTAAIYASRAELKPLLFEGWANDIAAGGQLTITTD 106
QY 59 VENPFGPTGIMGIDLDNCRQAQSVRFGTNISETVTEVDFSAARPRVTSSTTVLADTV 118
DB 107 VENPFGPEGLIGDIVEKFKQSERFGTTFTETVKNVDFSSKPKLFTDSRTVLADSV 166
QY 119 VVATGAVARRLHFGSDT-----YNNRGISACAVCDGAAPFRNKPIAVIGGDSAMEEGN 174
DB 167 IISTGAVAKRLSFTSGGNGGFWNRGISACAVCDGAAPFRNKPLVVIIGGDSAMEEAN 226

QY 175 FLTKYGSQVYIIHRRNTFRASKINQARALSNPKIQVWVDSVVEAYGAGGGPLAGVKV 234
DB 227 FLTKYGSQVYIIHRRNTFRASKINQARALSNPKIEVWNSAVVEAYGAGGGPLAGVKV 286
QY 235 NLVTGEVSDLVQVSLGFLFAIGHEPATKFLNGQLEHADGYVATKPGSTHISVEGVFAAGDV 294
DB 287 NVVTGVDVSLKVSGLFPAIGHEPATKFLDGLQLEDEDEGYVATKPGSTHISVEGVFAAGDV 346
QY 295 QDKYRQAITAAGSGCMAALDAEHLQEVGAQVQKSD 331
DB 347 QDKYRQAITAAGSGCMAALDAEHLQEVGAQVQKSD 383

RESULT 12

US-10-141-531-105
; Sequence 105, Application US/10141531
; Publication No. US20030100743A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Lugimbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 105
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Arabidopsis thaliana variant
US-10-141-531-105

Query Match 78.2%; Score 1334.5; DB 14; Length 383;
Best Local Similarity 76.0%; Pred. No. 2.1e-126;
Matches 256; Conservative 39; Mismatches 33; Indels 9; Gaps 2;

QY 4 SAAAPL-----RTRVCIIIGSGPAAHTAAIYASRAELKPVLFEGWMANDIAAGGQTTTTD 58
DB 47 SAAAVDMETHKTKVCIIVGSGPAAHTAAIYASRAELKPVLFEGWMANDIAAGGQTTTTD 106
QY 59 VENPFGPTGIMGIDLMNCRAQSVREGTNILSETVTEVDFSPARFVTSSTTVLADTV 118
DB 107 VENPFGPEGLGIDIVEKFRKQSERFGTTITFTVNVKDFSSKPKFLTDSRTVLADSV 166
QY 119 VVATGAVARLHFGSDT----YNNRGISACVCDGAAPIFRNKPIAVIGGDSAMEGN 174
DB 167 IISTGAVAKLSFTSGEGNGGFWNRGISACVCDGAAPIFRNKPLVWIGGDSAMEAN 226
QY 175 FLTKYGSQVYIIHRRNTFRASKINQARALSNPKIQVWVDSVVEAYGAGGGPLAGVKV 234
DB 287 NVVTGVDVSLKVSGLFPAIGHEPATKFLDGLQLEDEDEGYVATKPGSTHISVEGVFAAGDV 346
QY 295 QDKYRQAITAAGSGCMAALDAEHLQEVGAQVQKSD 331
DB 347 QDKYRQAITAAGSGCMAALDAEHLQEVGAQVQKSD 383

RESULT 13

US-10-290-072-150
; Sequence 150, Application US/10290072
; Publication No. US2003021151A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Lugimbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-3
; CURRENT APPLICATION NUMBER: US/10/290,072

US-10-141-531-141
; Sequence 141, Application US/10141531
; Publication No. US20030100743A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Lugimbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 141
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Arabidopsis thaliana variant
US-10-141-531-141

Query Match 78.2%; Score 1334.5; DB 14; Length 383;
Best Local Similarity 76.0%; Pred. No. 2.1e-126;
Matches 256; Conservative 39; Mismatches 33; Indels 9; Gaps 2;

QY 4 SAAAPL-----RTRVCIIIGSGPAAHTAAIYASRAELKPVLFEGWMANDIAAGGQTTTTD 58
DB 47 SAAAVDMETHKTKVCIIVGSGPAAHTAAIYASRAELKPVLFEGWMANDIAAGGQTTTTD 106
QY 59 VENPFGPTGIMGIDLMNCRAQSVREGTNILSETVTEVDFSPARFVTSSTTVLADTV 118
DB 107 VENPFGPEGLGIDIVEKFRKQSERFGTTITFTVNVKDFSSKPKFLTDSRTVLADSV 166
QY 119 VVATGAVARLHFGSDT----YNNRGISACVCDGAAPIFRNKPIAVIGGDSAMEGN 174
DB 167 IISTGAVAKLSFTSGEGNGGFWNRGISACVCDGAAPIFRNKPLVWIGGDSAMEAN 226
QY 175 FLTKYGSQVYIIHRRNTFRASKINQARALSNPKIQVWVDSVVEAYGAGGGPLAGVKV 234
DB 287 NVVTGVDVSLKVSGLFPAIGHEPATKFLDGLQLEDEDEGYVATKPGSTHISVEGVFAAGDV 286
QY 235 NLVTGEVSDLVQVSLGFLFAIGHEPATKFLNGQLEHADGYVATKPGSTHISVEGVFAAGDV 294
DB 287 NVVTGVDVSLKVSGLFPAIGHEPATKFLDGLQLEDEDEGYVATKPGSTHISVEGVFAAGDV 346
QY 295 QDKYRQAITAAGSGCMAALDAEHLQEVGAQVQKSD 331
DB 347 QDKYRQAITAAGSGCMAALDAEHLQEVGAQVQKSD 383

RESULT 14

US-10-290-072-150
; Sequence 150, Application US/10290072
; Publication No. US2003021151A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Lugimbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-3
; CURRENT APPLICATION NUMBER: US/10/290,072

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; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/376,682
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 150
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Arabidopsis thaliana variant
US-10-290-072-150

Query Match      78.2%; Score 1333.5; DB 12; Length 383;
Best Local Similarity 76.0%; Pred. No. 2.7e-126;
Matches 256; Conservative 39; Mismatches 33; Indels 9; Gaps 2;

QY      4 SAAAPL-----RFRVCIIGSGPAAHTAAIYAAPAEKLPVLFEQWMANDIAAGQLTITTD 58
Db      47 SAAAADVMTETKTKVCIVGSGPAAHTAAIYASRAELKPLLFEGWMANDIAFGGQLTITTD 106
QY      59 VENFPFGPTGIMGIDLMDCRAQSVRFGTNLSLSETVTEVDFSGARPPRVTSSTTVLADTV 118
Db      107 VENFPFGPEGLGIDIVEKFKQSEREGTTFITETVNVKVDFFSKPKLFTDSRTVLADSV 166
QY      119 VVATGAVARLHFSGSDT-----YWNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEBN 174
Db      167 IISTGAVAKRLSFTGSGEGNGGFWMRGISACAVCDGAAPIFRNKPLVVIIGGDSAMEBAN 226
QY      175 FLTKYGSQVYIIHRRNTFRASKIMOARALSNPKIQVWVDSEVVEAYGAGGGLAGVKVK 234
Db      227 FLTKYGSKVYIIHRFTDFNASKIMOQALSNPKIEVWNSAVVEAYGDENGRVLGGLVKV 286
QY      235 NLVTGEVSDIQVSGLFFAIGHPEPATKFLNGQLELHADGYVATKPGSTHTSVGVFAAGDV 294
Db      287 NVVTGVDVSLKVSGLFFAIGHPEPATKFLDQGLELDEDDGYVTKPGTTKTSVGVFAAGDV 346
QY      295 QDKKYRQAITAAGSGCMAALDAEHYLOEVGAQVGKSD 331
Db      347 QDKKYRQAITAAGTGCMAALDAEHYLOEIGSQEGKSD 383

RESULT 15
US-10-141-531-150
; Sequence 150, Application US/10141531
; Publication No. US20030100743A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Luginbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioresdoxin Reductase Activity
; FILE REFERENCE: A-71457-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/141,531
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 150
; LENGTH: 383
; TYPE: PRT
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Arabidopsis thaliana variant
US-10-141-531-150

Query Match      78.2%; Score 1333.5; DB 14; Length 383;
Best Local Similarity 76.0%; Pred. No. 2.7e-126;
Matches 256; Conservative 39; Mismatches 33; Indels 9; Gaps 2;

QY      4 SAAAPL-----RFRVCIIGSGPAAHTAAIYAAPAEKLPVLFEQWMANDIAAGQLTITTD 58
Db      47 SAAAADVMTETKTKVCIVGSGPAAHTAAIYASRAELKPLLFEGWMANDIAFGGQLTITTD 106
QY      59 VENFPFGPTGIMGIDLMDCRAQSVRFGTNLSLSETVTEVDFSGARPPRVTSSTTVLADTV 118
Db      107 VENFPFGPEGLGIDIVEKFKQSEREGTTFITETVNVKVDFFSKPKLFTDSRTVLADSV 166
QY      119 VVATGAVARLHFSGSDT-----YWNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEBN 174
Db      167 IISTGAVAKRLSFTGSGEGNGGFWMRGISACAVCDGAAPIFRNKPLVVIIGGDSAMEBAN 226
QY      175 FLTKYGSQVYIIHRRNTFRASKIMOARALSNPKIQVWVDSEVVEAYGAGGGLAGVKVK 234
Db      227 FLTKYGSKVYIIHRFTDFNASKIMOQALSNPKIEVWNSAVVEAYGDENGRVLGGLVKV 286
QY      235 NLVTGEVSDIQVSGLFFAIGHPEPATKFLNGQLELHADGYVATKPGSTHTSVGVFAAGDV 294
Db      287 NVVTGVDVSLKVSGLFFAIGHPEPATKFLDQGLELDEDDGYVTKPGTTKTSVGVFAAGDV 346
QY      295 QDKKYRQAITAAGSGCMAALDAEHYLOEVGAQVGKSD 331
Db      347 QDKKYRQAITAAGTGCMAALDAEHYLOEIGSQEGKSD 383

Search completed: June 21, 2004, 14:07:39
Job time : 49 secs
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OM protein - protein search, using sw model

Run on: June 21, 2004, 13:45:47 ; Search time 22 Seconds
(without alignments)
779.083 Million cell updates/sec

Title: US-10-091-841A-9

Perfect score: 1706

Sequence: 1 MEGSAAAPLRTVCIIGSGP.....ALDAHYLQEVGAQVKSDZ 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pdp.*
- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pdp.*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pdp.*
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- 5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pdp.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1706	100.0	332	4	US-09-540-014-9
2	1469	86.1	310	4	US-09-598-747-27
3	1296	76.0	333	4	US-09-598-747-25
4	1250.5	73.3	332	4	US-09-540-014-24
5	948	55.6	334	1	US-08-386-729A-7
6	910.5	53.4	311	4	US-09-198-452A-331
7	707.5	41.5	320	4	US-09-328-352-5678
8	697.5	40.9	317	4	US-09-328-352-8114
9	688	40.3	349	4	US-09-489-039A-12096
10	684.5	40.1	339	4	US-09-543-681A-5633
11	677	39.7	323	4	US-09-252-991A-29849
12	674	39.5	321	4	US-09-540-014-25
13	542.5	31.8	310	4	US-09-134-000C-5514
14	458	26.8	329	4	US-09-134-000C-3897
15	410.5	24.1	300	4	US-09-598-747-7
16	401.5	23.5	508	4	US-09-134-001C-4570
17	400.5	23.5	215	4	US-09-252-991A-31700
18	397.5	23.3	538	4	US-09-543-681A-4490
19	382.5	22.4	253	4	US-09-134-001C-5512
20	373.5	21.9	510	1	US-08-220-677A-2
21	369.5	21.7	523	4	US-09-328-352-6394
22	369.5	21.7	523	4	US-09-328-352-6395
23	368.5	21.6	512	4	US-09-107-532A-6559
24	365	21.4	301	4	US-09-598-747-6
25	350.5	20.5	522	4	US-09-252-991A-28463
26	323	18.9	524	4	US-09-540-236-2706
27	316.5	18.6	199	4	US-09-252-991A-31441

28	266.5	15.6	192	4	US-09-489-039A-13402	Sequence 13402, A
29	252.5	14.8	339	4	US-09-107-532A-6420	Sequence 6420, Ap
30	197	11.5	334	4	US-09-134-000C-5068	Sequence 5068, Ap
31	180.5	10.6	478	4	US-09-134-000C-5543	Sequence 5543, Ap
32	164.5	9.6	474	4	US-09-556-877-90	Sequence 90, Appl
33	164.5	9.6	474	4	US-09-620-412C-90	Sequence 90, Appl
34	164.5	9.6	474	4	US-09-410-588-90	Sequence 90, Appl
35	164.5	9.6	474	4	US-09-598-419-90	Sequence 90, Appl
36	154	9.0	87	4	US-09-134-001C-5497	Sequence 5497, Ap
37	151	8.9	474	4	US-09-328-352-7757	Sequence 7757, Ap
38	151	8.9	496	4	US-09-328-352-6168	Sequence 6168, Ap
39	150	8.8	564	2	US-08-878-957-32	Sequence 32, Appl
40	150	8.8	581	4	US-09-489-039A-11496	Sequence 11496, A
41	149.5	8.8	491	4	US-09-262-856A-5	Sequence 5, Appl
42	147	8.6	564	1	US-08-427-097-2	Sequence 2, Appl
43	147	8.6	564	1	US-08-427-097-14	Sequence 14, Appl
44	147	8.6	564	1	US-08-427-097-16	Sequence 16, Appl
45	147	8.6	564	1	US-08-427-097-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-09-540-014-9
; Sequence 9, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-540-014-9

Query Match	100.0%;	Score 1706;	DB 4;	Length 332;
Best Local Similarity	100.0%;	Pred. No. 1.1e-179;		
Matches 332;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MEGSAAPLRTVCIIGSGPAHTAAIYAARAEKPVLPFGWMANDIAAGQLTITDVE	60	
Db	1	MEGSAAPLRTVCIIGSGPAHTAAIYAARAEKPVLPFGWMANDIAAGQLTITDVE	60	
Qy	61	NFGPPTGIMIDMNCRAQSVFCNIISETVTEVDSARFRTVSDSTTVLADTVV	120	
Db	61	NFGPPTGIMIDMNCRAQSVFCNIISETVTEVDSARFRTVSDSTTVLADTVV	120	
Qy	121	ATGAVARLHFSGSDTYWNRGISACAVCDGAAPIFRNKPIAVTGGDSAMEEGNFKTKY	180	
Db	121	ATGAVARLHFSGSDTYWNRGISACAVCDGAAPIFRNKPIAVTGGDSAMEEGNFKTKY	180	
Qy	181	SOVYIIHRRNTFRASKIMQARALSNPKIQVWDSVEVYAGGGGGLAGYKVNLTGE	240	
Db	181	SOVYIIHRRNTFRASKIMQARALSNPKIQVWDSVEVYAGGGGGLAGYKVNLTGE	240	

QY 241 VSDLOVSGLFFAIGHEPATKFLNGOLELHADGYVATKPGSTHTSVGVEFAAGDVQDKKYR 300
DB 241 VSDLOVSGLFFAIGHEPATKFLNGOLELHADGYVATKPGSTHTSVGVEFAAGDVQDKKYR 300
QY 301 QAITAAGSCMAALDAHYLQEVGAQVGSZ 332
DB 301 QAITAAGSCMAALDAHYLQEVGAQVGSZ 332

RESULT 2

US-09-598-747-27
; Sequence 27, Application US/09598747
; Patent No. 6531648
; GENERAL INFORMATION:
; APPLICANT: Lananhan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gasdaska, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; TITLE OF INVENTION: THEREIN
; FILE REFERENCE: A-31383P1
; CURRENT APPLICATION NUMBER: US/09/598,747
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-598-747-27

Query Match 86.1%; Score 1469; DB 4; Length 310;
Best Local Similarity 91.6%; Pred. No. 1.5e-153;
Matches 283; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 1 MEGSAAAPTRVCIIGSGPAHTAIAAARAEKLVPEGWANDIAAGGQTTTTTVE 60
DB 1 MEGSAGAPLTRCIIGSGPSAHTAIAAARAEKLVPEGWANDIAAGGQTTTTTVE 60
QY 61 NFGPPTGIMIDLMDNCRAQSVFRTNLSLSEVDFSAFPRVTSSTVLADTVV 120
DB 61 NFGPPEGLIGLMDRCRAQSVFRTNLSLSEVDFSAFPRVTSSTVLADTVV 120
QY 121 ATCAVARLHFGSGDYVNRGISAACVCGAAPIFRNKPIAVIGGDSAMEGNFLTKYG 180
DB 121 ATCAVARLHFGSGDYVNRGISAACVCGAAPIFRNKPIAVIGGDSAMEGNFLTKYG 180
QY 181 SQVYIHRNTFRASKIMOARALSNPKIOVWDSVEVYAGGAGGGLAGVKNLVTGE 240
DB 181 SHVYIHRNTFRASKIMOARALSNPKIOVWDSVEVYAGGAGGGLAGVKNLVTGE 240
QY 241 VSDLOVSGLFFAIGHEPATKFLNGOLELHADGYVATKPGSTHTSVGVEFAAGDVQDKKYR 300
DB 241 VSDLOVSGLFFAIGHEPATKFLNGOLELHADGYVATKPGSTHTSVGVEFAAGDVQDKKYR 300
QY 301 QAITAAGSG 309
DB 301 QAITAAGSG 309

RESULT 3

US-09-598-747-25
; Sequence 25, Application US/09598747
; Patent No. 6531648
; GENERAL INFORMATION:
; APPLICANT: Lananhan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gasdaska, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; TITLE OF INVENTION: THEREIN
; FILE REFERENCE: A-31383P1
; CURRENT APPLICATION NUMBER: US/09/598,747
; CURRENT FILING DATE: 2000-06-21

; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-598-747-25

Query Match 76.0%; Score 1296; DB 4; Length 333;
Best Local Similarity 76.6%; Pred. No. 2e-134;
Matches 249; Conservative 33; Mismatches 39; Indels 4; Gaps 1;

QY 11 TRVCIIGSGPAHTAIAAARAEKLVPEGWANDIAAGGQTTTTTVDENPFGFTGIM 70
DB 9 TRVCIIGSGPAHTAIAAARAEKLVPEGWANDIAAGGQTTTTTVDENPFGFTGIM 68
QY 71 GIDLMDNCRAQSVFRTNLSLSEVDFSAFPRVTSSTVLADTVVATGAVARRLH 130
DB 69 GVELTDKFRKQSERFGTTFTETVTVKVDFSSKPKLFTDSKAILADAVILAIGAVAKWLS 128
QY 131 FSGSDT----YMRGISAACVCGAAPIFRNKPIAVIGGDSAMEGNFLTKYGSOVV 186
DB 129 FVSGEVLGGLMNRGISAACVCGAAPIFRNKPIAVIGGDSAMEGNFLTKYGSOVV 188
QY 187 HRRNTFRASKIMOARALSNPKIOVWDSVEVYAGGAGGGLAGVKNLVTGEVSDQV 246
DB 189 DRDADFASKIMOARALSNPKIOVWDSVEVYAGGAGGGLAGVKNLVTGEVSDQV 248
QY 247 SGLFFAIGHEPATKFLNGOLELHADGYVATKPGSTHTSVGVEFAAGDVQDKKYRQAITAA 306
DB 249 SGLFFAIGHEPATKFLNGOLELHADGYVATKPGSTHTSVGVEFAAGDVQDKKYRQAITAA 308
QY 307 GSGCMAALDAHYLQEVGAQVGSZ 331
DB 309 GTGCMAALDAHYLQEVGAQVGSZ 333

RESULT 4

US-09-540-014-24
; Sequence 24, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Callau, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-540-014-24

Query Match 73.3%; Score 1250.5; DB 4; Length 332;
Best Local Similarity 74.8%; Pred. No. 2.1e-129;
Matches 243; Conservative 33; Mismatches 44; Indels 5; Gaps 2;

QY 11 TRVCIIGSGPAHTAIAAARAEKLVPEGWANDIAAGGQTTTTTVDENPFGFTGIM 70

Db 9 TELCTVIGSPAAHTAAIYAARAEKPLLEFEGMWDIAAGGQLNPPR-ENFPGPPEGIL 67
QY 71 GIDLMDNCRAQSVRFGTNLSSTVTEVDFSPARPRVTSDSTTVLADTVVATGAVARRLH 130
Db 68 GVELDKFRKQSERFGTTFTETVTKVDFSSKPKLFTDSKAILADAVILAIGAVAKWLS 127
QY 131 FSGSDT----YVNRGISACVCDGAAPFRNKPIAVIGGDSAMEEGNFKTKYGSQVYII 186
Db 128 FVGSSEVLGGLNWRGISACVCDGAAPFRNKPIAVIGGDSAMEEGNFKTKYGSQVYII 187
QY 187 HERNTRFRASKINQARALSNPKIQVWVDSEVVEAYGAGGGLAGVKKVNLVTGEVSDIQV 246
Db 188 DRDADFASKINQARALSNPKIDVWNSVVEAYGGERDVLGGLKVKNNVTVGDVSDLVK 247
QY 247 SGLPFAIGHPATKFLNGOLELHAGGYATKPGSTHTSVGEVFAAGDVODKKYQAATAA 306
Db 248 SGLPFAIGHPATKFLDGGVELDSGYVVTKPTGTTQTSVPGVFAAGDVODKKYQAATAA 307
QY 307 GSGCMAALDAEHLQEVGAQVQKSD 331
Db 308 GIGCMAALDAEHLQEVGAQVQKSD 332

RESULT 5
US-08-386-729A-7
; Sequence 7, Application US/08386729A
; Patent No. 5753435
; GENERAL INFORMATION:
; APPLICANT: Aharonowitz, Yair
; APPLICANT: Van Der Voort, Lucia H. M.
; APPLICANT: Cohen, Gerald
; APPLICANT: Bovenberg, Roelof A. L.
; APPLICANT: Schreiber, Rachel
; APPLICANT: Argaman, Anat
; APPLICANT: Av-Gay, Yossef
; APPLICANT: Nan, Helena M.
; APPLICANT: Kattewilder, Alfred
; APPLICANT: Pallissa, Harriet
; TITLE OF INVENTION: An oxido reductase enzyme system
; TITLE OF INVENTION: obtainable from P. chrysogenum, the set of genes
; TITLE OF INVENTION: encoding the same and the use of oxido reductase enzyme
; TITLE OF INVENTION: systems or genes encoding the same for increasing antibiotic
; TITLE OF INVENTION: production
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weill, Gotshal & Manges
; STREET: 2882 Sand Hill Road, Ste. 280
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,729A
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/274,043
; FILING DATE: 12-JULY-1994
; APPLICATION NUMBER: US 07/820,688
; FILING DATE: 24-MARCH-1992
; APPLICATION NUMBER: PCT/NL91/000101
; FILING DATE: 18-JUNE-1991
; APPLICATION NUMBER: EP 90201598.1
; FILING DATE: 18-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter, Barbara
; REGISTRATION NUMBER: 32,750

REFERENCE/DOCKET NUMBER: GERO-024/02US
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-386-729A-7

Query Match 55.6%; Score 948; DB 1; Length 334;
Best Local Similarity 56.2%; Pred. No. 5.2e-96;
Matches 181; Conservative 62; Mismatches 71; Indels 8; Gaps 2;

QY 9 LRTVCIIGSPAAHTAAIYAARAEKPLLEFEGMWDIAAGGQLNPPR-ENFPGPPEGIL 68
Db 2 VHSKVLIIGSPGAAHTAAIYLRAEQVLYEGLNLANGTAAGGQLTTTDDVENFPFPFSG 61
QY 69 IMGIDLMDNCRAQSVRFGTNLSSTVTEVDFSPARPRVTSD-----STTVLADTVVVA 121
Db 62 IGGAEIAMDNRQAQSERFGTEIITETISKLDSRPFKMTWMDDEGSEPRVTADAVIA 121
QY 122 TGAVARRLHFSGSDTYWNRGISACVCDGAAPFRNKPIAVIGGDSAMEEGNFKTKYGS 181
Db 122 TGAVARRLNLPGSETYWNRGISACVCDGAAPFRNKPLYVIGGDSAAEAMFLAKYGS 181
QY 182 QVYTIHRRNTFRASKINQARALSNPKIQVWVDSEVVEAYG-GAGGGPPLAGVKVNLVTGE 240
Db 182 SVTVLVKDKLRSNINWADLLAHPKCKVFNVTATEVIGENKPNGLMTHLRVKDVLNSA 241
QY 241 VSDIQVSLGFLFAIGHPATKFLNGOLELHAGGYATKPGSTHTSVGEVFAAGDVODKKYR 300
Db 242 EEVVEANGFLYAVGHDPASGLVKGQVELDDGYIITKPGTSFTNVGVPACGVDQDKRYR 301
QY 301 QAITAAGSGCMAALDAEHLQEV 322
Db 302 QAITAAGSGCMAALDAEHLQEV 323

RESULT 6
US-09-198-452A-331
; Sequence 331, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 331
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-331

Query Match 53.4%; Score 910.5; DB 4; Length 311;
Best Local Similarity 55.1%; Pred. No. 6.4e-92;
Matches 173; Conservative 61; Mismatches 73; Indels 7; Gaps 3;

QY 9 LRTVCIIGSPAAHTAAIYAARAEKPLLEFEGMWDIAAGGQLTTTDDVENFPFPFSG 68
Db 2 IHSRLIIGSPGCTTAIYASRALHPLLEFEGFSG--ISGGQLMTTTEVENFPFPFSG 59
QY 69 IMGIDLMDNCRAQSVRFGTNLSSTVTEVDFSPARPRVTSDSTTVLADTVVATGAVARR 128
Db 60 ILGPKLMMNNKEQAVRFGTKTLAQDIISVDFSVRPFILKSEETYSQDCIATGASAKR 119
QY 129 LHF--SGSDTYWNRGISACVCDGAAPFRNKPIAVIGGDSAMEEGNFKTKYGSQVVI 186

Db 120 LPTGAGNDEFQWGVACAVCGASPIFKKOLYVIGGDSALEALYITRYGSHVVV 179
Qy 187 HRRNTFRASIMQARALNSPKIQVWMDSEVVEAYGGAGGGLAGVKVKMLVTGEVSDLOV 246
Db 180 HRRDKLRASKAMEARAQNEKITPLMNSIVKI---SGDSIVRSVDIKNVQTOEITREA 236
Qy 247 SGLFFAIGHPEPATKFLNGQLHLDHAGVATKPGSTHTSVGEVFAAGDVQDKKYRQAITAA 306
Db 237 AGVFFALGHKPDNTFLGGQLTDESGYIVTEKTSKTSVSVGAAGDVQDKKYRQAVTSA 296
Qy 307 GSGCMAALDAEHL 320
Db 297 GGGCMAALDAEHL 310

RESULT 7

US-09-328-352-5678
; Sequence 5678, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5678
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5678

Query Match 41.5%; Score 707.5; DB 4; Length 320;
Best Local Similarity 45.3%; Pred. No. 1.7e-69;
Matches 145; Conservative 57; Mismatches 101; Indels 17; Gaps 6;

Qy 11 TRVCIIGSGPAHAHTAAIYAARAEIKPVLFEQWMDANDIAAGGQLTTTDDVENFPFGPTGIM 70
Db 11 SRLIILGSGPAGYSAAYAAARANKPTLIAG-----LQGGQLTTTTEVDNWPDPGLT 65
Qy 71 GIDLMNCRQASVREGTINILSETVTEVDFSPRPVTSSTTVLADTVVATGAVARRLH 130
Db 66 GPALMDRMQAHAERFETELVYDHINEVDLNVRFVFKGDMEEYTCDALIIATGATAQVIG 125
Qy 131 FSGSDTYNWRGISACAVCDGGAAPFRNKPIAVIIGGDSAMEEGNFLT KYGSOVVIHRRN 190
Db 126 LESEQKFMGQGVSAACATCDGF--FYKNQVWVGGGNTAVEEALYLSNIAHVTLVHRD 183
Qy 191 TFRASKIMQARALNSP---KIQVWMDSEVVEAYGGAGGGLAGVKVKMLVTGEVSDLOVS 247
Db 184 SLRSEKILQDHLFAKEKGKISIVWNEVEEVLGDN TG--VTGVRKSTKDDSKQEVQVQ 241
Qy 248 GLFFAIGHPEPATKFLNGQLHLDHAGVATKPG-----SHTSVGEVFAAGDVQDKKYRQAI 303
Db 242 GLFIAIGHKPTSMFEGQLNLR--DGYIQVQSGTSGNATATSVAGVFAAGDVADSIYRQAI 300
Qy 304 TAAGSGCMAALDAEHLQEV 323
Db 301 TSAGSGCMAALDAEKLNL 320

RESULT 8

US-09-328-352-8114
; Sequence 8114, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 8114
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8114

Query Match 40.9%; Score 697.5; DB 4; Length 317;
Best Local Similarity 44.7%; Pred. No. 2.1e-68;
Matches 143; Conservative 60; Mismatches 100; Indels 17; Gaps 6;

Qy 11 TRVCIIGSGPAHAHTAAIYAARAEIKPVLFEQWMDANDIAAGGQLTTTDDVENFPFGPTGIM 70
Db 6 SRLIILGSGPAGYSAAYAAARANKPTLIAG-----LQGGQLTTTTEVDNWPDPGLT 60
Qy 71 GIDLMNCRQASVREGTINILSETVTEVDFSPRPVTSSTTVLADTVVATGAVARRLH 130
Db 61 GPALMDRMQAHAERFETELVYDHINEVDLNVRFVFKGDMEEYTCDALIIATGATAQVIG 120
Qy 131 FSGSDTYNWRGISACAVCDGGAAPFRNKPIAVIIGGDSAMEEGNFLT KYGSOVVIHRRN 190
Db 121 LESEQKFMGQGVSAACATCDGF--FYKNQVWVGGGNTAVEEALYLSNIAHVTLVHRD 178
Qy 191 TFRASKIMQARALNSP---SNPKIQVWMDSEVVEAYGGAGGGLAGVKVKMLVTGEVSDLOVS 247
Db 179 SLRSEKILQDHLFAKEKGKISIVWNEVEEVLGDN TG--VTSVRKSTQDESQKQDEVEH 236
Qy 248 GLFFAIGHPEPATKFLNGQLHLDHAGVATKPG-----SHTSVGEVFAAGDVQDKKYRQAI 303
Db 237 GLFVAIGHKPTSMFEGQLNLR--DGYIQVQSGTSGNATATSVAGVFAAGDVADSIYRQAI 295
Qy 304 TAAGSGCMAALDAEHLQEV 323
Db 296 TSAGSGCMAALDAEKLQDL 315

RESULT 9

US-09-489-039A-12096
; Sequence 12096, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12096
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12096

Query Match 40.3%; Score 688; DB 4; Length 349;
Best Local Similarity 45.9%; Pred. No. 2.8e-67;
Matches 146; Conservative 61; Mismatches 93; Indels 18; Gaps 7;

Qy 11 TRVCIIGSGPAHAHTAAIYAARAEIKPVLFEQWMDANDIAAGGQLTTTDDVENFPFGPTGIM 70
Db 34 SKLLIILGSGPAGYTAAYAAARANKLPVLITG-----MEKGGQLTTTTEVENWPGDNDLT 88
Qy 71 GIDLMNCRQASVREGTINILSETVTEVDFSPRPVTSSTTVLADTVVATGAVARRLH 130
Db 89 GPLLMERMEHAKEFETEIFHISVDLQNRFPFRUTGDSGEYTCDALIIATGASARYIG 148
Qy 131 FSGSDTYNWRGISACAVCDGGAAPFRNKPIAVIIGGDSAMEEGNFLT KYGSOVVIHRRN 190
Db 149 LPSEEAFFKRGVSAACATCDGF--FYKNQVWVGGGNTAVEEALYLSNIAHVTLVHRD 206

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191   TFRASKIMQARAL-----SNPKIQVVDSEVVEAYGGAGGGLAGVKYANLVGTGE-VSDLOV 244
      :|||:|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
207   SFRAEKILIKRLMDKVSAGNTVLHTDRTLLEVTGDQMGG--VSGRLRDTFNNDNVESLEV 264
      :|||:|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
247   SLGFALGAHEPATKFLNQLLEHADGYVATKPG-----STHTSVEGVFAAGDVQDKKYROA 302
      :|||:|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
265   AGLFVAIGHSPNTAFEGQLELE-NGYIKVQSIGHGNATQTSLPGVFAAGDVMDHIYROA 323
      :|||:|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
303   ITAAGSGCMALDAEHYL 320
      :|||:|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
324   ITSAGTGCMAALDAERYL 341
      :|||:|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 10
US-09-543-681A-5633
; Sequence 5633, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEIN
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5633
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5633
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						Gaps	6;

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DB	18	EVSMSITIKHSLIILIGSGPAGTAAYAAARANLEPVLITG-----VEKGGQLTTTTEVEN	72
QY	62	PGFPTGIMGIDLMDNCBQAQSVRFCNTILSETTVEDFSARPPRVTSSTTVLADTVVVA	121
DB	73	WPGDEPLGTGPGLDMDMTQHAEEKFTEIISDHINKVDLKNRFFRLFGDEQEYTCDAIIA	132
QY	122	TGAVARRHLSGSDTYWNRGTSACAVCDGAAPIFRANKPIAVTIGGSDSAWEEGNFLTKEYS	181
DB	133	TCASARYICLGPSEEAFAKKGVSACATCDGF--FYRNQVAVVVGNGTAVEEALYLANIAS	190
QY	182	QYVYIHRNTRFRASKIMQARAL----SNPKIOVWDSVEVVEAVGGAGGCGPLAGVKVKNIWT	238
DB	191	EVHLIHRRDSFRSEKILIDRLMDKVNGNIILHTDRTIDEVLGDDMG--VTKVRLKDTKS	248
QY	239	GEVSDIQVSGSLFPAIGCHEPATKFLNGQLHLAGDYVATKPG---SHTSVEGVFAAGDV	294
DB	249	DKTEEEVMGVFIAIGHSNTSIFEDQALD-NGYIKVQSGTQGNATQTSIEGVFAAGDV	307
QY	295	QKKYTRQAITAAGSGCMAALDAEHYL	320
DB	308	MDHYRQAITSAAGTGCMAALDAERYL	333

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RESULT 11
US-09-252-991A-29849
; Sequence 29849, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

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[illegible]

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RESULT 12
US-09-540-014-25
; Sequence 25, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillau, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-540-014-25

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Best Local Similarity 45.3%; Pred. No. 8.5e-66;

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Best Local Similarity		34.2%;	Pred. No. 9.2e-37;		
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Db	4	VAIIGGGPAGLTAALYSARYGLKTVFFE-----TVDPVSQLSLAAKIENYFGEPS--GM	56		
Qy	73	DLMDNCRAQSVRFCTNILSETVTVEVDFSAERPRVTSSTTVLADTVVATGAVARRLHFS	132		
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Qy	133	GSDTYMNRGISACAVCDGAAPIFRNKPIAVIGGDSAMEEGNFLT KYGSQVYIIHRNTF	192		
Db	117	GESAFIGRGVSYCATCG--NFFRGKKVIVVSGKEAIEDAIVLHDIGCEVTIVSRTPSF	174		
Qy	193	RASKIMQARALSNPKIQVWDSEVVEAYGGAGGGLAGVKVKNLVTGEVSDLOVSGLFFA	252		
Db	175	RAEKAL-VEEVEKRGIPVHYSTTIRKI---IGSGKVKVWAYNREKKEFEIEADGIFVA	230		
Qy	253	IGHEPATKFLNGOLELHAD--GYVATKPGSTHTSVEGVFAAGDVQDKKYRQAITAAGSGC	310		
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Search completed: June 21, 2004, 14:02:47
Job time : 23 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2004, 19:44:11 ; Search time 505 Seconds
(without alignments)
3011.726 Million cell updates/sec

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Perfect score: 1706
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
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Database : Published Applications NA:
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13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2*
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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ALIGNMENTS

RESULT 1

US-10-091-841-10
; Sequence 10, Application US/10091841
; Publication No. US20030150010A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/10/091,841
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21

1	1628	95.4	995	15	US-10-091-841-10	Sequence 10, Appl
2	1628	95.4	995	15	US-10-091-841-23	Sequence 23, Appl
3	1581	92.7	1286	13	US-10-425-114-5073	Sequence 5073, Ap
4	1581	92.7	1286	13	US-10-425-114-3716	Sequence 3716, Ap
5	1469	86.1	1560	15	US-10-306-292-26	Sequence 26, Appl
6	1346.5	78.9	1152	9	US-09-938-842A-2486	Sequence 2486, Ap
7	1346.5	78.9	1152	11	US-09-938-842A-2486	Sequence 2486, Ap
8	1324	77.6	1002	9	US-09-897-898-1	Sequence 1, Appl
9	1324	77.6	1002	9	US-09-897-898-2	Sequence 2, Appl
10	1324	77.6	1002	13	US-09-897-425-36	Sequence 36, Appl
11	1324	77.6	1002	13	US-09-897-425-37	Sequence 37, Appl
12	1324	77.6	1002	15	US-10-032-201B-8	Sequence 8, Appl
13	1324	77.6	1002	15	US-10-032-201B-10	Sequence 10, Appl
14	1324	77.6	1344	13	US-10-290-072-238	Sequence 238, App
15	1324	77.6	3787	9	US-09-897-898-13	Sequence 13, Appl
16	1324	77.6	3787	13	US-09-897-425-48	Sequence 48, Appl
17	1324	77.6	3787	15	US-10-032-201B-22	Sequence 22, Appl
18	1324	77.6	4545	9	US-09-897-898-18	Sequence 18, Appl
19	1324	77.6	4545	13	US-09-897-425-53	Sequence 53, Appl
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21	1324	77.6	4546	9	US-09-897-898-15	Sequence 15, Appl
22	1324	77.6	4546	13	US-09-897-425-50	Sequence 50, Appl
23	1324	77.6	4546	15	US-10-032-201B-24	Sequence 24, Appl
24	1324	77.6	6357	13	US-10-290-072-38	Sequence 38, Appl
25	1324	77.6	6357	13	US-10-290-072-42	Sequence 42, Appl
26	1324	77.6	6357	15	US-10-141-531-38	Sequence 38, Appl
27	1324	77.6	6357	15	US-10-141-531-42	Sequence 42, Appl
28	1312	76.9	6357	13	US-10-290-072-35	Sequence 35, Appl
29	1312	76.9	6357	13	US-10-290-072-45	Sequence 45, Appl
30	1312	76.9	6357	15	US-10-141-531-35	Sequence 35, Appl
31	1312	76.9	6357	13	US-10-141-531-45	Sequence 45, Appl
32	1311	76.8	6357	13	US-10-290-072-37	Sequence 37, Appl
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35	1310	76.8	6357	13	US-10-290-072-34	Sequence 34, Appl
36	1310	76.8	6357	13	US-10-290-072-40	Sequence 40, Appl
37	1310	76.8	6357	13	US-10-290-072-44	Sequence 44, Appl
38	1310	76.8	6357	15	US-10-141-531-34	Sequence 34, Appl
39	1310	76.8	6357	15	US-10-141-531-40	Sequence 40, Appl
40	1310	76.8	6357	13	US-10-141-531-44	Sequence 44, Appl
41	1309	76.7	6357	13	US-10-290-072-43	Sequence 43, Appl
42	1309	76.7	6357	13	US-10-290-072-46	Sequence 46, Appl
43	1309	76.7	6357	15	US-10-141-531-43	Sequence 43, Appl
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; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-10-091-841-10

Alignment Scores:
Pred. No.: 4,55e-196 Length: 995
Score: 1628.00 Matches: 328
Percent Similarity: 98.80% Conservative: 0
Best Local Similarity: 98.80% Mismatches: 3
Query Match: 95.43% Indels: 3
DB: 15 Gaps: 0

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DB 61 GCGCGCACACGCGCGCCATCTACGCGCCCGCGGAGCTCAAGCCGCTCTTCGAG 120
QY 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrThrThrThr 60
DB 121 GGTGTGATGGCCACACGATCCGCGCGGGGCGGAGCTCACCACACCGAGCTCGAG 180
QY 61 AsnPheProGlyPheProThrGlyLeuMetGlyIleMetGlyIleAspLeuMetAspAsnCysArgAla 80
DB 181 AACTTCCCGGATTCGCCACCGCATATGGGCGATCGACCTCATGGACAACTTCGCGGCC 240
QY 81 GlnSerValArgPheGlyThrIleLeuSerGluThrValThrGluValAspPheSer 100
DB 241 CAGTCGTCCGCTTCGGACCAACATCTCTTCGAGACCGTCACCGAGGTGACATTCCTCC 300
QY 101 AlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrValValVal 120
DB 301 GCGCGGCCCTTCGCGCTCACTCCGACTCCACACCGCTCCGCGGACACCGCTCGCTGCTC 360
QY 121 AlaThrGlyValAlaAlaArgArgLeuHisPheSerGlySerAspThrTyrTrpAsnArg 140
DB 361 GCCACGGGCGCGCTCGCGCGCGCTCCATTTCTCCGGTTCGACACCTTACTTGGAACCGC 420
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
DB 421 GGCATCTCCGCTCGCGCTCTCGACGCGGCTCGGCCATCTTCGGGAACAAGCCCATC 480
QY 161 AlaValIleGlyGlyAspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGly 180
DB 481 GCGGTTCATCGCGCGCGGTGATTCGCGCATGGAGGAAGCAACTTCTCACCAGTACGGA 540
QY 181 SerGlnValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
DB 541 TCCCAAGTGTACATCATCCACGGCGCAACACCTTCGCGGCTCCCAAGATTATCGAGCT 600
QY 201 ArgAlaLeuSerAsnProLysIleGlnValValTrpAspSerGluValValGluAlaTyr 220
DB 601 AGGGCGCTCTCCAATCTTAAGTCCAGGTGTGTGGACTC-GAGGTCTCGAGGCTTAC 659
QY 221 GlyGlyValGlyGlyProLeuAlaGlyValLysValLysAsnLeuValThrGlyGlu 240
DB 660 GCGGTGTGAGCGCGGCCCATATGCTGGGTCAAGTCAAGACTTGTGTGTGTGTGTGTG 719
QY 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
DB 720 GTGTCTGACCTTCAGGTGTTCGGGCTTTTCTTCGCCATCGGCGCATGAGCGGCCCAAG 779
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DB 780 TTCTCTCAATGGGCGAGCTTGAGCTCCGATGGGTATGTGGCCACCAAGCGGGCTCT 839
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RESULT 2
; Sequence 23, Application US/10091841
; Publication No. US20030150010A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioresdoxin and
; TITLE OF INVENTION: NADP-Thioresdoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/10/091,841
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-10-091-841-23

Alignment Scores:
Pred. No.: 4,55e-196 Length: 995
Score: 1628.00 Matches: 328
Percent Similarity: 98.80% Conservative: 0
Best Local Similarity: 98.80% Mismatches: 3
Query Match: 95.43% Indels: 3
DB: 15 Gaps: 0

US-10-091-841A-9 (1-332) x US-10-091-841-23 (1-995)

QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgValCysIleIleGlySerGlyPro 20
DB 1 ATGGAGGATCCCGCGCGCGCTCCGACACGGGTGTGCATCATCGCAGCGGCCG 60
QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
DB 61 GCGCGCACACGCGCGCCATCTACGCGCCCGCGGAGCTCAAGCCGCTCTTCGAG 120
QY 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrThrThrThr 60
DB 121 GGTGTGATGGCCACACGATCCGCGCGGGGCGGAGCTCACCACACCGAGCTCGAG 180
QY 61 AsnPheProGlyPheProThrGlyLeuMetGlyIleMetGlyIleAspLeuMetAspAsnCysArgAla 80
DB 181 AACTTCCCGGATTCGCCACCGCATATGGGCGATCGACCTCATGGACAACTTCGCGGCC 240

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Qy 201 ArgAlaLeuSerAsnProLysIleGlnValValTrpAspSerGluValValGluAlaTyr 220
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Db 780 TTCTCTCAATCGGAGCTTGAGTCCATCGCGATGGGTATGTGGCCACCAAGCGGCGCTC 839
Qy 281 ThrHisThrSerValGluGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg 300
Db 840 ACACATACCAAGTGTGGAGGGGTC-TTGTGCTGTGGAGAGCTGAGGATTAAGATATCT 998
Qy 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu-AspAlaGluHisTyrLe 320
Db 899 CAGGCCATTACTGCTGCTGGATCAGGTTGCATGGCTGCTTTGGAGCGCGGAGCACTATCT 958
Qy 320 uGlnGluValGlyAlaGlnValGlyLysSerAsp 331
Db 959 GCAGGAGTGGTGACACAGGTGGGCAAGTCTGAT 992

RESULT 3
US-10-425-114-5073
; Sequence 5073, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5073
; LENGTH: 1286
; TYPE: DNA
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; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 700447274_FLI

US-10-425-114-5073

Alignment Scores:

Pred. No.:	5,99e-190	Length:	1286
Scores:	1581.00	Matches:	304
Percent Similarity:	95.17%	Conservative:	11
Best Local Similarity:	91.84%	Mismatches:	16
Query Match:	92.67%	Indels:	0
DB:	13	Gaps:	0

US-10-091-841A-9 (1-332) x US-10-425-114-5073 (1-1286)

```
Qy 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgValCysIleIleGlySerGlyPro 20
Db 58 ATGAGGGATCCGGCGCGCTCCGCTCCGACGGCGATCTGCATCATCGGAGCGGTC 117
Qy 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
Db 118 GCTGCGCACACGGCAGCATCTACGCGCGCGCGGAGCTCAAGCTGTGCTCTCGAG 177
Qy 41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
Db 178 GCTGCGATGGCAACGACATCGCGCGGGCGGCGAGCTCACCAACCCAGCGCTCGAG 237
Qy 61 AsnPheProGlyPheProThrGlyIleMetGlyIleAspLeuMetAspAsnCysArgAla 80
Db 238 AACTTCCGGGCTTCCCAACGGCATCATGGCGCGCGACCTATGGACAACTGCGCGCG 297
Qy 81 GlnSerValArgPheGlyThrAsnIleLeuSerGluThrValThrGluValAspPheSer 100
Db 298 CAGTCTCCGCTTGGCACCACCAATCTCTCCGAGACCGCTCACCGCGCTGACCTTCG 357
Qy 101 AlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrValVal 120
Db 358 GCCTGCCCATTCGAGTTAGTGAGACTCCCAACCGCTCTCCGCGGATCGCGTTATCGTT 417
Qy 121 AlaThrGlyAlaValAlaAlaArgArgLeuHisPheSerGlySerAspThrTyrTrpAsnArg 140
Db 418 GCCACGGAGCGCTCGCGCGCGCTCCACTTCCCGCGGTCGATGCATCTGGAACCGC 477
Qy 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProfile 160
Db 478 GGCATCTCCGCTGTGCGCTCTGTGAGCGTCCGCCGCCCATCTTCCGTAACAGCCCATC 537
Qy 161 AlaValIleGlyGlyIleAspSerAlaMetGluGlyGlyAsnPheLeuThrLysTyrGly 180
Db 538 GCCGTATAGCGCGCGGCGACTCCGCTATGGAGGAGTCCAATTTCTCCCAAGTACGCG 597
Qy 181 SerGlnValTyrIleIleHisArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 598 TCCACGCTCATCATCATCCACCGCGCAATACCTTCCGTGCTTCCAGATCATGAGGCC 657
Qy 201 ArgAlaLeuSerAsnProLysIleGlnValValTrpAspSerGluValValGluAlaTyr 220
Db 658 AGGCGCTTGAGAACCCCAAAATTAAGTCTCTCTGGACTCGAAGTTGTGAGGCCAT 717
Qy 221 GlyGlyAlaGlyGlyProLeuAlaGlyValLysValLysAsnLeuValThrGlyGlu 240
Db 718 GCGCGCGCAAAACGGCGGCCCATTTGGTGGCTAAAGGTTAAGAACCTACTGAATGGT 777
Qy 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 778 GTCTCGATCTTCAAGTGTCTGGGCTCTTCTTCCGCAATCGGCGCATGAGCGCGCA 837
Qy 261 PheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySer 280
Db 838 TTCTGGCGGACAGCTTGAACCTCGATTCAGATGTTATGTGGAACCAACAGCCAGTTCC 897
Qy 281 ThrHisThrSerValGluGlyValPheAlaAlaGlyAspValGlnAspLysTyrArg 300
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Db 898 ACTCACACAGTGTAAAGGGTGTATTGCTGCTGGCGACGTCGACGACGAAGAAGTACCGT 957
Qy 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeu 320
Db 958 CAGGCCATTACTCCCGCTGGATCAGGGTGCATGGCTGCAATGGACGCTGAGCACTACCTG 1017
Qy 321 GlnGluValGlyAlaGlnValGlySerAsp 331
Db 1018 CAGGAGATCGGTGCACAGGAGGGAAAGTCTGAT 1050
RESULT 4
US-10-425-114-3716
; Sequence 3716, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3716
; LENGTH: 1325
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700336177_FLI
US-10-425-114-3716
Alignment Scores:
Pred. No.: 6,26e-190 Length: 1325
Score: 1581.00 Matches: 304
Percent Similarity: 95.17% Conservative: 11
Best Local Similarity: 91.84% Mismatches: 16
Query Match: 92.67% Indels: 0
DB: 13 Gaps: 0
US-10-091-841A-9 (1-332) x US-10-425-114-3716 (1-1325)
Qy 1 MetGluGlySerAlaAlaProLeuArgThrArgValCysIleIleGlySerGlyPro 20
Db 87 ATGAGGGATCCGGCGCGCTCCGCTCCGACGCGCATCTGCATCATCGGGAGCGGTCCC 146
Qy 21 AlaAlaHisThrAlaAlaIleThrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
Db 147 GCTGGCACAGCGAGCCCATCTACGGCGCCCGCGGAGCTCAAGCTGTGCTTTCGAG 206
Qy 41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrAspValGlu 60
Db 207 GGCTGGATGGCAACGACATCGCGCGGGCGGCGAGCTCACCAACCAACCGACGTCGAG 266
Qy 61 AsnPheProGlyPheProThrGlyTleMetGlyIleAspLeuMetAspAsnCysAtqAla 80
Db 267 AACTTCCCGGCTTCCCAACAGGATCATGGCGCGCGACCTCATGGACAATGCCGCGCG 326
Qy 81 GlnSerValArgPheGlyThrAsnIleLeuSerGluThrValThrGluValAspPheSer 100
Db 327 CAGTCCCTGCGCTTTGGCAACCAACATCTCTCCGAGACCGTCACCGCGCTGCTTTTCG 386
Qy 101 AlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrValVal 120
Db 387 GCCTGCCCATTCGAGTGTAGTGACACTCCCAACCGCTCTCGCGGATCGCGTATCGTT 446
Qy 121 AlaThrGlyAlaValAlaArgArgLeuHisPheSerGlySerAspThrThrTyrTrpAsnArg 140
Db 447 GCCACGGGAGCGCTCGCGCGGCGCTCCACTTCCCGGGTCCGATCGACTACTGGAAACCGC 506

Qy 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
Db 507 GGCATCTCCGCTGTGGCGTCTGTGACGGTGCCGCCCATCTTCCTGTAACAAGCCCATC 566
Qy 161 AlaValIleGlyGlyGlyAspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGly 180
Db 567 CCGCTCATAGCGGGCGGCGACTCCGCTATGGAGGAGTCCAAATTTCTCCCAAGTACGGC 626
Qy 181 SerGlnValTyrIleIleHisArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 627 TCCACGCTCTACATCATCCACGCGCAATACCTTCGCTGCTTCCAAAGATCATCAGGCC 686
Qy 201 ArgAlaLeuSerAsnProLysIleGlnValValTyrPheSerGluValValGluAlaTyr 220
Db 687 AGGCGCTTGAGAACCCCAAAATTAAGTCTCTGGGACTCGGAAGTTGTGAGGCGCTAT 746
Qy 221 GlyGlyAlaGlyGlyGlyProLeuAlaGlyValLysValLysAsnLeuValThrGlyGlu 240
Db 747 GCGCGCGCAACGCGCGGCCCATTCGCTGGCGTAAGGTTAAGAACCTACTCAATGGTGA 806
Qy 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 807 GTCTCGGATCTTCAGTGTCTGGCTCTTCTGCCCATCGGCGCATGAGCCGCGACCAA 866
Qy 261 PheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySer 280
Db 867 TTCTCTGGGCGGACAGCTTGAACCTCGATTGATGTTATGTGGAACCAAGCCAGGTTC 926
Qy 281 ThrHisThrSerValGluGlyValPheAlaAlaGlyAspValGlnAspLysIleTyrArg 300
Db 927 ACTCACACAGTGTAAAGGGTGTATTGCTGCTGGCGACGTGCGAGCAAGAAAGTACCGT 986
Qy 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeu 320
Db 987 CAGGCCATTACTCCGCTGGATCAGGGTGCATGGCTGCTGATTCGACGCTGAGCACTACCTG 1046
RESULT 5
US-10-306-292-26
; Sequence 292, Application US/10306292
; Publication No. US20030145347A1
; GENERAL INFORMATION:
; APPLICANT: Lananhan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gasdaska, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; FILE REFERENCE: THEREIN
; FILE REFERENCE: A-31383P1
; CURRENT APPLICATION NUMBER: US/10/306,292
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US/09/598,747
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-306-292-26
Alignment Scores:
Pred. No.: 1,24e-175 Length: 1560
Score: 1469.00 Matches: 283
Percent Similarity: 95.47% Conservative: 12
Best Local Similarity: 91.59% Mismatches: 14
Query Match: 86.11% Indels: 0
DB: 15 Gaps: 0
US-10-091-841A-9 (1-332) x US-10-306-292-26 (1-1560)

QY 1 MetGluGlySerAlaAlaProLeuArgThrArgValCysIleIleGlySerGlyPro 20
DB 406 ATGAGGGATCCGCGGGGCGCGCTCCGACCGCGCTGTCATCATCGGAGCGGGCG 465
QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
DB 466 TCGCGGACACGGCGGGGATCTACGCGCGCGCGGGAGCTCAAGCCGTCCTTCGAG 525
QY 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
DB 526 GGTGGTTCGCAACGACATCGCGCGGGGGCGAGCTCACACCCACCCAGCGTCGAG 585
QY 61 AsnPheProGlyPheProThrGlyIleMetGlyIleAspLeuMetAspAsnCysArgAla 80
DB 586 AACTTCCCGGGTTCCCGAGGGATCTCGCGCGGAGCTCATGATCGTCCGCGGC 645
QY 81 GlnSerValArgPheGlyThrAsnIleLeuSerGlnThrValThrGluValAlaAspPheSer 100
DB 646 CAGTCCCTCCGGTTCGCGACCGACGATCATCTCCGAGACCGTCAACCGCTCTCTCC 705
QY 101 AlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrValVal 120
DB 706 GCCCGCCCTTCCCGCTCGCTCCGACTCCACACCGCTGCTGCCGCGAGCGCTCGTC 765
QY 121 AlaThrGlyAlaValAlaArgLeuHisPheSerGlySerAspThrThrTyrAsnArg 140
DB 766 GCCACCGCGCGCTCGCGCGGACTCCACTTCGCGGCTCCGACGCTACTCGAACCGC 825
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
DB 826 GGCATCTCAGCTCGCGCTCGCGAGCGGCGCCGCAATCTTCAGAACACCAACCCATC 885
QY 161 AlaValIleGlyGlyGlyAspSerAlaMetGluGlyAsnPheLeuThrLysTyrGly 180
DB 886 CGCGTCACTCGCGCGGCGACTCCGCGCATGAGGAGTCCAACTTCCTCACCAGTACGGC 945
QY 181 SerGlnValTyrIleIleHisArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
DB 946 TCCCATGTGTATCATCATCCACCGCGCAACCTTCGCGCGCTCCAGATCATGACGGCC 1005
QY 201 ArgAlaLeuSerAsnProLysIleGlnValValTyrAspSerGluValAlaGluAlaTyr 220
DB 1006 AGGGGTGTTCACACCCCAAGATCCAGTTTCTGGGACTCTGAGTCTCGCGGCTCTAC 1065
QY 221 GlyGlyAlaGlyGlyProLeuAlaGlyValLysValLysAsnLeuValThrGlyGlu 240
DB 1066 GCGCGGAGGTGGAGGTCCATGCTGCTGCTCAAGGTGAAGACTTGGTTACTTGGGAAG 1125
QY 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
DB 1126 ATCTCCGACCTTCAGGTTCGCTGCTCTTCCTCGCCATCGGACATGAACCGCGACGAG 1185
QY 261 PheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySer 280
DB 1186 TTTTCGCGGGGAGCTTTCAGTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1245
QY 281 ThrHisThrSerValGluGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg 300
DB 1246 ACGCACACAGTGTGAAGGGGTCTTCTGCTGCGGGATGTGCGAGGACAGAGTATCGC 1305
QY 301 GlnAlaIleThrAlaAlaGlySerGly 309
DB 1306 CAGGCTATTACTCGCGCTGGATCAGGT 1332

RESULT 6
US-09-938-842A-2486
; Sequence 2486, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krebs, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2486
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-2486
Alignment Scores:
Pred. No.: 2,66e-160 Length: 1152
Score: 1346.50 Matches: 258
Percent Similarity: 88.13% Conservative: 39
Best Local Similarity: 76.56% Mismatches: 31
Query Match: 78.93% Indels: 9
DB: 9 Gaps: 2
US-10-091-841A-9 (1-332) x US-09-938-842A-2486 (1-1152)
QY 4 SerAlaAlaAlaProLeu-----ArgThrArgValCysIleIleGlySer 18
DB 139 TCGCGCGCGCGCGCTCGACATCGAAACTCACAACCCAGTTTGCATCGCGAGT 198
QY 19 GlyProAlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeu 38
DB 199 GGACGACGACGACACACGCGCGGATCTATGTCATCGAGCGGAGCTTAAAGCTCTCTC 258
QY 39 PheGluGlyTyrMetAlaAsnAspIleAlaGlyGlyGlnLeuThrThrThrThrAsp 58
DB 259 TTCGAAGGATGATGCTTAACGATCGCTCCCGCGGTCAATTAACACACACCGAC 318
QY 59 ValGluAsnPheProGlyPheProThrGlyIleMetGlyIleAspLeuMetAspAsnCys 78
DB 319 GTCGAAACTTCCCTGGGTTCCTGAAGGTATCTCGGTATTGATATCGTGAGAAATTC 378
QY 79 ArgAlaGlnSerValArgPheGlyThrAsnIleLeuSerGluThrValThrGluValAsp 98
DB 379 AGAAACAACTCGAGAGATTCGAACTACGATCTTCACGGAACCTGTTCACAAAGTTGAT 438
QY 99 PheSerAlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrVal 118
DB 439 TTCTCATCGAAACCGTTTAAGCTATTCTGATTCGAGAACTGTTCGCTGATTCGTGA 498
QY 119 ValValAlaThrGlyAlaValAlaAlaArgArgLeuHisPheSerGlySerAspThr----- 136
DB 499 ATCATTTCTACTGGAGCTGTTCCTAAACGCTCTAGCTTCACCTGGATCTCGTGAAGTAA 558
QY 137 -----TyrTyrAsnArgGlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIle 154
DB 559 GGTGGTTTGGATCGTGTATCTCCGCTTGTGCTGTTTGGACGAGCTGCTCCGATT 618
QY 155 PheArgAsnLysProIleAlaValIleGlyGlyAspSerAlaMetGluGlyAsn 174
DB 619 TTTAGGAATAAGCCTCTCTGCTTATTGCTGTGTGATTCAGCTATGAGGAAAGCGAAT 678
QY 175 PheLeuThrLysTyrGlySerGlnValTyrIleIleHisArgAsnThrPheArgAla 194
DB 679 TTTCTGACTAAGTATGATCTAGGTTTATATTAATCATAGGAGGATACGTTTAGGGCG 738
QY 195 SerLysIleMetGlnAlaAlaArgAlaLeuSerAsnProLysIleGlnValValTyrAspSer 214
DB 739 TCTAAGATTATGCAGCAGAGAGCTTTGCTCAACCTTAAGATTGAAGTATTGGAACCTCT 798
QY 215 GluValValGluAlaTyrGlyGlyAlaGlyGlyGlyProLeuAlaGlyValLysValLys 234


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Score: 1324.00 Matches: 252
Percent Similarity: 88.00% Conservative: 34
Best Local Similarity: 77.54% Mismatches: 35
Query Match: 77.61% Indels: 4
DB: 9 Gaps: 1

US-10-091-841A-9 (1-332) x US-09-897-898-2 (1-1002)

QY 11 ThrArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
DB 25 ACAAGGCTCTGTATCGTAGAAGTGGCCGACACACACGGCGGCGATTACGCAGCT 84
QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaGly 50
DB 85 AGGCTGAACCTTAAACCTCTCTCTCGAAGGATGGTAAACGACATCGCTCCCGGT 144
QY 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProThrGlyLeuMet 70
DB 145 GGTCAACTAACCAACCAACCCAGCTCGAGATTTCCTCCGAGATTTCAGAGGATTCTC 204
QY 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
DB 205 CGAGTAGAGCTCACTGACAAATTCGTAACATCGGAGCGATTTCGGTACTACGATATT 264
QY 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
DB 265 ACAGAGACGGTGACAAAAGTGGATTCTCTCTCGAAACCGTTTAAGCTATTACAGATTCA 324
QY 111 ThrThrValLeuAlaAspThrValValAlaThrGlyValAlaAlaArgArgLeuHis 130
DB 325 AAAGCCATTCTCGTACGCTGTGATTCTCGTACTGGAGCTGGCTAAGCGGCTTAGC 384
QY 131 Phe-----SerGlySerAspThrThrTrpAsnArgGlyIleSerAlaCysAla 146
DB 385 TTCGTTGGATCTGCTGAAGTCTCGAGGTTCTCGAACCCTGGAATCTCCGCTTGCT 444
QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
DB 445 GTTTCGACGAGCTGCTCGCATATTCGTAACAACTCTTCGCGGTGATCGGTGGAGGC 504
QY 167 AspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGlySerGlnValTyrIle 186
DB 505 GATTTCAGCAATGGAAGAAGCAAACTTTCTACAAATATGGAATCTAAAGTGTATATATC 564
QY 187 HisArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuSerAsnPro 206
DB 565 CATAGGAGAGATGCTTTTAGAGCGCTCTAAGATTATGACGACGCGAGCTTTGTCTAATCCT 624
QY 207 LysIleGlnValValTyrAspSerGluValValGluAlaTyrGlyGlyAlaGlyGly 226
DB 625 AAGATTGATGTGATTGGAACCTCTGTTGTGGAAGCTTATGGAGATGAGAAAGAGAT 684
QY 227 ProLeuAlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnVal 246
DB 685 GTGCTTGAGGATGGAAGTGAAGATGTGGTACCGGAGATGTTTCTGATTATAAAGTT 744
QY 247 SerGlyLeuPheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeu 266
DB 745 TCTGGATTGTTCTTGTATTGTCATGACCGCAGCTACCAAGTTTTCGATGTTGGTGTGT 804
QY 267 GluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerValGlu 286
DB 805 GAGTTAGATTCCGATGTTTATGTTGTCCAGAAAGCTGCTGCTACTACACAGACTAGCTTCC 864
QY 287 GlyValPheAlaAlaGlyAspValGluAspLysTyrArgGlnAlaIleThrAlaAla 306
DB 865 CGAGTTTCGCTGCGGTGATGTTCCAGATTAAGAATATAGGCAAGCCATCATCTGCTGCA 924
QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnValGlyAlaGln 326
DB 925 GGAACCTGGTGCATGGCAGCTTTGGATGTCAGAGCATTACTTACAAGAGATTGGATCTCAG 984
QY 327 ValGlyLysSerAsp 331

Db 985 CAAGGTAAGAGTGAT 999

RESULT 10
US-09-897-425-36
; Sequence 36, Application US/09897425
; Publication No. US20020088025A1
; GENERAL INFORMATION:
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMIA, BIPIN K.
; TITLE OF INVENTION: PREPARATION OF THIOREDOXIN AND THIOREDOXIN REDUCTASE
; TITLE OF INVENTION: PROTEINS ON OIL BODIES
; FILE REFERENCE: 034547/0106
; CURRENT APPLICATION NUMBER: US/09/897,425
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/210,843
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/846,021
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/366,783
; PRIOR FILING DATE: 1994-12-30
; PRIOR APPLICATION NUMBER: 08/142,418
; PRIOR FILING DATE: 1993-11-16
; PRIOR APPLICATION NUMBER: 07/659,835
; PRIOR FILING DATE: 1991-02-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Published NADPH
; OTHER INFORMATION: thioredoxin reductase sequence
; NAME/KEY: CDS
; LOCATION: (1) ... (999)
US-09-897-425-36

Alignment Scores:
Pred. No.: 154e-157 Length: 1002
Score: 1324.00 Matches: 252
Percent Similarity: 88.00% Conservative: 34
Best Local Similarity: 77.54% Mismatches: 35
Query Match: 77.61% Indels: 4
DB: 13 Gaps: 1

US-10-091-841A-9 (1-332) x US-09-897-425-36 (1-1002)

QY 11 ThrArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
DB 25 ACAAGGCTCTGTATCGTAGAAGTGGCCGACACACACGGCGGCGATTACGCAGCT 84
QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaGly 50
DB 85 AGGCTGAACCTTAAACCTCTCTCTCGAAGGATGGTAAACGACATCGCTCCCGGT 144
QY 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProThrGlyLeuMet 70
DB 145 GGTCAACTAACCAACCAACCCAGCTCGAGATTTCCTCCGAGATTTCAGAGGATTCTC 204
QY 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
DB 205 CGAGTAGAGCTCACTGACAAATTCGTAACATCGGAGCGATTTCGGTACTACGATATT 264
QY 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
DB 265 ACAGAGACGGTGACAAAAGTGGATTCTCTCTCGAAACCGTTTAAGCTATTACAGATTCA 324
QY 111 ThrThrValLeuAlaAspThrValValAlaThrGlyValAlaAlaArgArgLeuHis 130
DB 325 AAAGCCATTCTCGTACGCTGTGATTCTCGTACTGGAGCTGGCTAAGCGGCTTAGC 384
QY 131 Phe-----SerGlySerAspThrThrTrpAsnArgGlyIleSerAlaCysAla 146
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QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGlyAlaGln 326
 Db 925 GGAAGTGGTGCATGGAGCGCTTTGGATGCGAGCATTAATACAGAGATTGGATCTCAG 984
 QY 327 ValGlyLysSerAsp 331
 Db 985 CAAGGTAAGAGTGAT 999

RESULT 12

US-10-032-201B-8
 ; Sequence 8, Application US/10032201B
 ; Publication No. US20030167524A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Rooijen, Gijls
 ; APPLICANT: Deckers, Harm
 ; APPLICANT: Heifetz, Peter Bernard
 ; APPLICANT: Briggs, Steven
 ; APPLICANT: Dalmia, Bipin Kumar
 ; APPLICANT: Del Val, Greg
 ; APPLICANT: Zaplachinski, Steve
 ; APPLICANT: Moloney, Maurice
 ; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
 ; FILE REFERENCE: 38814 351B
 ; CURRENT APPLICATION NUMBER: US/10/032,201B
 ; CURRENT FILING DATE: 2001-12-19
 ; NUMBER OF SEQ ID NOS: 313
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 1002
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-10-032-201B-8

Alignment Scores:
 Pred. No.: 1.54e-157 Length: 1002
 Score: 1324.00 Matches: 252
 Percent Similarity: 88.00% Conservative: 34
 Best Local Similarity: 77.54% Mismatches: 35
 Query Match: 77.61% Indels: 4
 DB: 15 Gaps: 1

US-10-091-841A-9 (1-332) x US-10-032-201B-8 (1-1002)

QY 11 ThrArgValCysIleleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
 Db 25 ACAAGGCTGTATGTCGAGGAATGGCCGACACACGCGCGGATTTACGCGAGCT 84
 QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
 Db 85 AGGGCTGAACCTTAACCTCTCTCTTCGAAGGATGGCTAACGACATCGCTCCCGT 144
 QY 51 GlyGluLeuThrThrThrAspValGluAsnPheProGlyPheProThrGlyIleMet 70
 Db 145 GGTCAACTAACACACACACGCGCGAGATTTCCCGGATTTCCAGAGGATTTCTC 204
 QY 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
 Db 205 CGAGTAGAGCTCACTGACAAATTCCTTAACATCGAGCGATTCGGTACTACGATATT 264
 QY 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
 Db 265 ACAGACCGGTGACGAAGTCGATTTCTCTCGAAACCGTTTAAGACGATTTACAGATTCA 324
 QY 111 ThrThrValLeuAlaAspThrValValAlaThrGlyValAlaValAlaArgLeuHis 130
 Db 325 AAAGCCATTCTGCTGACCTGTGATTCCTCGTACTGAGCTGTGGTAAAGCGGTTAGC 384
 QY 131 Phe-----SerGlySerAspThrTyrTyrAsnArgGlyIleSerAlaCysAla 146
 Db 385 TTGCTTGGATCTGGTGAAGGTTCTGGAGGTTCTCGAACCGTGAATCTCCGCTTGCT 444
 QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166

Db 445 GTTTCGACGAGAGTGCCTCCGATATTCGTAACAAACCTCTTCGGGTGATCGGTGAGGC 504
 QY 167 AspSerAlaMetGluGluGlyAsnPheLeuThrIleTyrGlySerGlnValTyrIleIle 186
 Db 505 GATTCAGCAATGGAAGAAGCAAACTTCTTACAAATATGGATCTAAAGTGTATATAATC 564
 QY 187 HisArgArgAsnThrPheArgAlaSerIleMetGlnAlaArgAlaLeuSerAsnPro 206
 Db 565 CATAGGAGAGATGCTTTTAGAGCGCTTAAGATTATGAGCAGCAGCGAGCTTTGCTAATCCT 624
 QY 207 LysIleGlnValValTrpAspSerGluValValGluAlaTyrGlyAlaGlyGlyGly 226
 Db 625 AAGATTGATGATTGGAACTCGTCTCTTGTGAAGCTTATGGAGATGGAGAAGAGAT 684
 QY 227 ProLeuAlaGlyValLysValLysValLysValThrGlyGluValSerAspLeuGlnVal 246
 Db 685 GTGCTTCGAGGATTGAAAGTGAAGATGTGTGTACGAGGCTGTCTGATTTAAAGTT 744
 QY 247 SerGlyLeuPhePheAlaIleGlyHisGluProIleThrIlePheLeuAsnGlyGlnLeu 266
 Db 745 TCTGATTTGTTCTTGTCTTATTTGGTCATGAGCCAGCTACCAAGTTTTTGGATGGTGGT 804
 QY 267 GluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerValGlu 286
 Db 805 GAGTTAGATTCCGATGGTTATGTTGTACGAGGCTGTGTACTACACAGCTAGCGTCCC 864
 QY 287 GlyValPheAlaAlaGlyAspValGlnAspLysIleTyrArgGlnAlaIleThrAlaAla 306
 Db 865 GGAGTTTTCGCTCGGGTGATGTTTCAGATTAAGAGATATAGGCAAGCCATCCTCCTGCA 924
 QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGlyAlaGln 326
 Db 925 GGAAGTGGTGCATGGAGCGCTTTGGATGCGAGCATTAATACAGAGATTGGATCTCAG 984

RESULT 13

US-10-032-201B-10
 ; Sequence 10, Application US/10032201B
 ; Publication No. US20030167524A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Rooijen, Gijls
 ; APPLICANT: Deckers, Harm
 ; APPLICANT: Heifetz, Peter Bernard
 ; APPLICANT: Briggs, Steven
 ; APPLICANT: Dalmia, Bipin Kumar
 ; APPLICANT: Del Val, Greg
 ; APPLICANT: Zaplachinski, Steve
 ; APPLICANT: Moloney, Maurice
 ; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
 ; FILE REFERENCE: 38814 351B
 ; CURRENT APPLICATION NUMBER: US/10/032,201B
 ; CURRENT FILING DATE: 2001-12-19
 ; NUMBER OF SEQ ID NOS: 313
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10
 ; LENGTH: 1002
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1002)
 ; OTHER INFORMATION: cDNA encoding NADPH thioredoxin reductase
 US-10-032-201B-10

Alignment Scores:
 Pred. No.: 1.54e-157 Length: 1002
 Score: 1324.00 Matches: 252
 Percent Similarity: 88.00% Conservative: 34

Best Local Similarity: 77.54% Mismatches: 35
 Query Match: 77.61% Indels: 4
 DB: 15 Gaps: 1

US-10-091-841A-9 (1-332) x US-10-032-201B-10 (1-1002)

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QY 11 ThrArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
DB 25 ACAAGGCTCTGTATCGTAGAGAGTGGCCCGGCGCACACACGCGGGCGATTACGAGCT 84
QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
DB 85 AGGCTGAACCTTAAACCTCTCTCTCGAAGATGGATGCTAACGACATCGCTCCCGGT 144
QY 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProThrGlyIleMet 70
DB 145 GGTCACTTAACAACACCGAGCTGAGAAATTCCTCCGGAATTCGAGAGGTATCTC 204
QY 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
DB 205 GGAGTAGAGCTCACTGACAAATTCGTAACAATCGGAGCGATTCGGTACTACGATATT 264
QY 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
DB 265 ACAGAGCGGTGAGAGAGTGGATTCCTTCGAAACCGTTTAAGCTATTACAGATTCA 324
QY 111 ThrThrValLeuAlaAspThrValValAlaThrGlyValAlaAlaArgArgLeuHis 130
DB 325 AAAGCCATTCCTCGTACGCTGTGATTCGCTACTCGAGCTGTGGCTAAGCGGCTTAGC 384
QY 131 Phe-----SerGlySerAspThrTyrTrpAsnArgGlyIleSerAlaCysAla 146
DB 385 TTCGTGGATCTGGTAGAGTTCGGAGGTTCTCGAACCGTGGAAATCTCCGCTTGCT 444
QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
DB 445 GTTTCGACGAGCTGCTCCGATATTCGTAACAACCTCTTCGGGTGATCGGTGAGGC 504
QY 167 AspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGlySerGlnValTyrIle 186
DB 505 GATTTCAGCAATGGAAGAGCAAACTTCTTACAAATATGATCTAAAGTGTATATAATC 564
QY 187 HisArgArgAsnThrPheArgAlaSerIleMetGlnAlaArgAlaLeuSerAsnPro 206
DB 565 CATAGGAGATGCTTTTAGAGCTCTAAGATTATGACGACGAGCTTTGTCTAATCCT 624
QY 207 LysIleGlnValValTrpAspSerGluValValGluAlaTyrGlyAlaGlyGly 226
DB 625 AAGATTGATGTGATTGGAACCTGCTGTTGTGAAGCTTATGGAGATGGAAGAGAT 684
QY 227 ProLeuAlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnVal 246
DB 685 GTGCTTGAGGATGGAAGTGAAGATGTGGTTTACCGGAGATGTTCTGTATTTAAAGTT 744
QY 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeu 266
DB 745 TCTGGATTGTTCTTGTCTATTGTTGTCATGAGCCAGCTACCAAGTTTGTGGATGGTGGTT 804
QY 267 GluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerValGlu 286
DB 805 GAGTTAGATTCCGATGGTATTGTTGTCACGAAGCTCGTACTACACAGCTAGCGTTCCC 864
QY 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
DB 865 GGAGTTTTCGTCGGGTGATGTTTCAGATTAAGATATAGGCAAGCCATCACTGCTGCA 924
QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGlyAlaGln 326
DB 925 GGAATCGGTGATGCGAGCTTGGATGACAGCATTTACTTACAAGAGATTGGATCTCAG 984
QY 327 ValGlyLysSerAsp 331
DB 985 CAAGGTAAGATGAT 999

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RESULT 14

US-10-290-072-238
 ; Sequence 238, Application US/10290072
 ; Publication No. US20030211511A1
 ; GENERAL INFORMATION:

; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Dalmia, Bipin K.
 ; APPLICANT: del Val, Greg
 ; APPLICANT: Desjardis, John R.
 ; APPLICANT: Heifetz, Peter
 ; APPLICANT: Luginbuhl, Peter
 ; APPLICANT: Muchhal, Umesh

; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity

; FILE REFERENCE: A-71457-3
 ; CURRENT APPLICATION NUMBER: US/10/290,072

; CURRENT FILING DATE: 2002-11-06
 ; PRIOR APPLICATION NUMBER: US 60/370,609

; PRIOR FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: US 60/376,682

; PRIOR FILING DATE: 2002-04-29
 ; PRIOR APPLICATION NUMBER: US 10/141,531

; PRIOR FILING DATE: 2002-05-06
 ; PRIOR APPLICATION NUMBER: US 60/289,029

; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 239

; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 238

; LENGTH: 1344

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: synthetic

US-10-290-072-238

Alignment Scores:

Prod. No.: 2 37e-157 Length: 1344
 Score: 1324.00 Matches: 252
 Percent Similarity: 88.00% Conservative: 34
 Best Local Similarity: 77.54% Mismatches: 35
 Query Match: 77.61% Indels: 4
 DB: 13 Gaps: 1

US-10-091-841A-9 (1-332) x US-10-290-072-238 (1-1344)

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QY 11 ThrArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
DB 367 ACAAGGCTCTGTATCGTAGAGTGGCCCGGCGCACACACGCGGGCGATTACGAGCT 426
QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
DB 427 AGGCTGAACCTTAAACCTCTCTTCGAGATGGATGGCTAACGACATCGCTCCCGT 486
QY 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProThrGlyIleMet 70
DB 487 GGTCAACTAACCAACACCGAGCTCGAGATTTCCCGGATTTCCAGAAAGTATTCTC 546
QY 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
DB 547 GGAGTAGAGCTCACTGACAAATTCGTAACAATCGGAGCGGATTCGGTACTACGATATT 606
QY 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
DB 607 ACAGAGCGGTGACGAAAGTCGATTCTCTTCGAAACCGTTTAAGCTATTACAGATTCA 666
QY 111 ThrThrValLeuAlaAspThrValValAlaThrGlyAlaValAlaArgGluHis 130
DB 667 AAGGCCATTCCTCGCTGAGCGCTGTGATTCTCGCTACTCGAGCTGTGGCTAAGCGGTTAGC 726
QY 131 Phe-----SerGlySerAspThrTyrTrpAsnArgGlyIleSerAlaCysAla 146
DB 727 TTCGTGGATCTGGTGAAGGTTCTGAGGATTTCTGGAACCGTGGAAATCTCCGCTTGCT 786

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QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
DB 787 GTTTCGACGAGCTGCTCCGATATTCGTAACAACCTTTCGGTGTATCGGTGGAGGC 846
QY 167 AspSerAlaMetGluGlyCysPheLeuThrLysTyrGlySerGlnValTyrIle 186
DB 847 GATTTCAGCATGGAAGACCAACCTTCTCAAAATATGATCTAAAGTGTATATAATC 906
QY 187 HisArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuSerAsnPro 206
DB 907 CATAGGAGAGATGCTTTAGAGCGTCTAAGATTATGACGACGAGCTTTGCTAATCCT 966
QY 207 LysIleGlnValValTyrAspSerGluValValGluAlaTyrGlyAlaGlyGly 226
DB 967 AAGATTGATGATTGGAACTCGCTGTGTGGAGCTTATGGAGATGGAGAAAGAGAT 1026
QY 227 ProLeuAlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnVal 246
DB 1027 GTGCTTGGAGGATTGAAGTGAAGATGTGTTACCGGAGATGTTCTGATTAAAGCTT 1086
QY 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeu 266
DB 1087 TCTGGATTGCTTTGCTATTGCTATGCTATGAGCAGCTACCAAGTTTTTGGATGGTGTGT 1146
QY 267 GluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerValGlu 286
DB 1147 GAGTTAGATTGGATGTTATGTTGTCAGAGCTGCTGACTACACAGCTAGCGTTCCC 1206
QY 287 GlyValPheAlaAlaGlyAspValGlnAspLysTyrArgGlnAlaIleThrAlaAla 306
DB 1207 GGAGTTTTCGCTGCGGTGATGTTTCAAGATAAGAGTATAGCCAGCCATCAGCTGCTCA 1266
QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGlyAlaGln 326
DB 1267 GGAAGTGGTGCATGGCAGCTTTGATGATGATGATGATGATGATGATGATGATGATG 1326
QY 327 ValGlyLysSerAsp 331
DB 1327 CAAGGTAAGATGAT 1341

RESULT 15

US-09-897-898-13
Sequence 13, Application US/09897898
Patent No. US20020037303A1
GENERAL INFORMATION:
APPLICANT: DECKERS, HARM M.
APPLICANT: VAN ROOIJEN, GIJS
APPLICANT: BOOTHE, JOSEPH
APPLICANT: GOLL, JANIS
APPLICANT: MOLONEY, MAURICE M.
APPLICANT: DALMIA, BIPIN K.
TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
FILE REFERENCE: 034547/0104
CURRENT APPLICATION NUMBER: US/09/897,898
CURRENT FILING DATE: 2001-09-21
PRIORITY FILING DATE: 2000-05-24
PRIORITY FILING DATE: 1999-11-24
PRIORITY FILING DATE: 1998-05-27
PRIORITY FILING DATE: 1997-05-27
PRIORITY FILING DATE: 1997-05-27
PRIORITY FILING DATE: 1997-05-28
PRIORITY FILING DATE: 1998-02-25
PRIORITY FILING DATE: 1998-02-25
PRIORITY FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13

LENGTH: 3787
TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
NAME/KEY: CDS
LOCATION: (1555)..(2553)
OTHER INFORMATION: Description of Unknown Organism: Phaseolin
OTHER INFORMATION: promoter-thioredoxin reductase-phaseolin
OTHER INFORMATION: terminator
US-09-897-898-13
Alignment Scores:
Pred. No.: 1,08e-156 Length: 3787
Score: 1324.00 Matches: 252
Percent Similarity: 88.00% Conservative: 34
Best Local Similarity: 77.54% Mismatches: 35
Query Match: 77.61% Indels: 4
DB: 9 Gaps: 1
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QY 11 ThrArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
DB 1579 ACAAGGCTCTGTATCTAGGAAGTGGCCAGCGGCACACACGCGCGGATTTACGAGCT 1638
QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaGly 50
DB 1639 AGGCTGAACTTAAACCTCTCTCTTGAAGAGATGGTAAACACATCGCTCCCGT 1698
QY 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProThrGlyIleMet 70
DB 1699 GGTCAACTAACACACACACCGAGCTCGAGATTTCCCGGATTTCCAGAGGATATTC 1758
QY 71 GlyLeuAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
DB 1759 GGAGTAGCTACTGACAAATTCCTGAAACATCGGAGCGATTCGGTACTACGATATTT 1818
QY 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
DB 1819 ACAGAGCGGTGACGAAAGTCGATTTCTCTCGAAGACCGTTTAAGCTATTCACAGATTC 1878
QY 111 ThrThrValLeuAlaAspThrValValValAlaThrGlyAlaValAlaArgArgLeuHis 130
DB 1879 AAGCCATTCTCGCTGACGCTGTGATTTCTCGCTACTGAGAGCTGTGGCTAAGCGGCTTAG 1938
QY 131 Phe-----SerGlySerAspThrTyrTrpAsnArgGlyIleSerAlaCysAla 146
DB 1939 TTCGTTGGATCTGGTGAAGGTTCTGAGGTTTCTGGAACCGTGGATCTCCGCTTGTGCT 1998
QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
DB 1999 GTTTCGACGAGCTGCTCCGATATTTCCGTAACAAACCTTTCGGTGTATCGGTGGAGGC 2058
QY 167 AspSerAlaMetGluGlyCysPheLeuThrLysTyrGlySerGlnValTyrIleIle 186
DB 2059 GATTTCAGCATGGAAGACCAACCTTCTCAAAATATGATCTAAAGTGTATATAATC 2118
QY 187 HisArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuSerAsnPro 206
DB 2119 CATAGGAGAGATGCTTTAGAGCGTCTAAGATTATGACGACGAGCTTTGCTAATCCT 2178
QY 207 LysIleGlnValValTyrAspSerGluValValGluAlaTyrGlyAlaGlyGly 226
DB 2179 AAGATTGATGATTGGAACTCGCTGTGTGGAGAGCTTATGGAGATGGAGAAAGAGAT 2238
QY 227 ProLeuAlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnVal 246
DB 2239 GTGCTTGGAGGATTGAAGTGAAGATGTGTTACCGGAGATGTTTCTGATTAAAGTT 2298
QY 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeu 266
DB 2299 TCTGGATTGTTCTTCTGCTATTGCTATGATGATGATGATGATGATGATGATGATGATG 2358

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Qy 267 GluLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerValGlu 286
Db 2359 GAGTTAGATTCGGATGGTTATGTGTACAGAGCCTGGTACTACACAGACTAGCGTCCC 2418
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
Db 2419 GGAGTTTTCGCTGGGGTGATGTTTCAGGATAAGAGTATAGGCCAAGCCATCACTGCTGCA 2478
Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGlyAlaGln 326
Db 2479 GGAACCTGGGTGCATGGCAGCTTTGGATGCCAGACATTACTTACAGAGATTGGATCTCAG 2538
Qy 327 ValGlyLysSerAsp 331
Db 2539 CAAGGTAAGAGTGAT 2553
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Search completed: June 21, 2004, 21:10:34
Job time : 511 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2004, 18:37:01 ; Search time 89 Seconds
(without alignments)

2070.154 Million cell updates/sec

Title: US-10-091-841A-9

Perfect score: 1706

Sequence: 1 MEGSAAPLRTRVCIIIGSP.....ALDAEHLQEVGAQVGRSDZ 332

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1628	95.4	995	4	US-09-540-014-10
2	1628	95.4	995	4	US-09-540-014-23
3	1469	86.1	1560	4	US-09-598-747-26
4	1296	76.0	1021	4	US-09-598-747-24
5	1223.5	71.7	998	4	US-09-540-014-26
6	910.5	53.4	1230025	4	US-09-198-452A-1
7	895.5	52.5	1423	1	US-08-386-729A-6
8	720	42.8	1443	1	US-09-221-017B-685
9	723	42.4	4403765	3	US-09-103-840A-2
10	723	42.4	4411529	3	US-09-103-840A-1
11	707.5	41.5	963	4	US-09-328-352-1552
12	707.5	41.5	49617	4	US-09-596-002-28

Alignment Scores:

Pred. No.: 2.5e-178 Length: 995
Score: 1628.00 Matches: 328
Percent Similarity: 98.80% Conservative: 0
Best Local Similarity: 98.80% Mismatches: 3

ALIGNMENTS

RESULT 1

US-09-540-014-10
; Sequence 10, Application US/09540014

; Patent No. 6380372

; GENERAL INFORMATION:

; APPLICANT: Cho, Myeong-Je

; APPLICANT: Del Val, Greg

; APPLICANT: Cailiau, Maxime

; APPLICANT: Lemauz, Peggy G.

; APPLICANT: Buchanan, Bob B.

; TITLE OF INVENTION: Barley Gene for Thioresdoxin and

; TITLE OF INVENTION: NADP-Thioresdoxin Reductase

; FILE REFERENCE: 2001-0701.30

; CURRENT APPLICATION NUMBER: US/09/540,014

; CURRENT FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: US 60/127,198

; PRIOR FILING DATE: 1999-03-31

; PRIOR APPLICATION NUMBER: US 60/169,162

; PRIOR FILING DATE: 1999-12-06

; PRIOR APPLICATION NUMBER: US 60/177,740

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: US 60/177,739

; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10

; LENGTH: 995

; TYPE: DNA

; ORGANISM: Hordeum vulgare

US-09-540-014-10

Query Match: 95.43% Indels: 3
DB: 4 Gaps: 0
US-10-091-841A-9 (1-332) x US-09-540-014-10 (1-995)
QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgValCysIlelleGlySerGlyPro 20
DB 1 ATGAGGGATCCGGCGGCGCCCTCCGACGCGGTGTGCATCATCGCAGCGGCCG 60
QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
DB 61 GCCGCGCACAGCGGCATCTACGCGCGCGCGGAGCTCAAGCGGTCTTCGAG 120
QY 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
DB 121 GGCTGGATGGCAACGACATCGCGCGCGCGGCGGAGCTCAAGCGGTCTTCGAG 120
QY 61 AsnPheProGlyPheProThrGlyLeuMetGlyLeuAspLeuMetAspAsnCysArgAla 80
DB 181 AACTTCCCGGATTCCTCCACCGGCATCTGGGATCGACCTCATGGACACTCCCGGCC 240
QY 81 GlnSerValArgPheGlyThrAsnIleLeuSerGluThrValThrGluValAspPheSer 100
DB 241 CAGTCCGTCGCTTCGGCACCAATCTCTCCGAGACCGCTCACCGAGGTCTCTCTCC 300
QY 101 AlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrValVal 120
DB 301 GCCCGCCCTTCGCGTCACTCGACTCCACACCGTCTCCGCGACCGGTCGTCGTC 360
QY 121 AlaThrGlyAlaValAlaArgLeuHisPheSerGlySerAspThrTyrTrpAsnArg 140
DB 361 GCCACGGCGCGCGCGCGCGCTCCATTTCTCGGTTCGACACCTACTTGGACCGC 420
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
DB 421 GGCATCTCCCGCTCGCGCGCTCGGCGCGCTCGCGCCCATCTTCGGACACAGCCCATC 480
QY 161 AlaValIleGlyGlyAspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGly 180
DB 481 GCGGTCACTCGCGCGCGGTGATTCGCGCATCGAGAGGCAACTCTCTACCAAGTACGA 540
QY 181 SerGlnValTyrIlelleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
DB 541 TCCCAAGTGACATCATCCACGGCGCGCAACACTTCCGCGCTCCCAAGATTATGACGGCT 600
QY 201 ArgAlaLeuSerAsnProLysIleGlnValValTyrAspSerGluValValGluAlaTyr 220
DB 601 AGGCGCTCTCCAATCTCAAGATCCAGTTGTCTGGGACTC-CAGGTCTCGAGGCTTAC 659
QY 221 GlyGlyAlaGlyGlyProLeuAlaGlyValLysValLysAsnLeuValThrGlyGlu 240
DB 660 GCGCGTGCAGCGCGCGCGCCCATTAGCTGGGGTCAAGGTCAAGAACTTGTGACTGTGAG 719
QY 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
DB 720 GTGTCTGACCTTCAGGTGTCCGGCTTTCTTCGCCATCGGCGATGAGCGCGCCACCAAG 779
QY 261 PheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySer 280
DB 780 TTTCTCAATGGGAGCTTGAGCTCCATGCGGATGGGTATGTGGCCACCAAGCGGCTCT 839
QY 281 ThrHisThrSerValGluGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg 300
DB 840 ACATATACCAAGTGTGGAGGGGTC-TTTGCTGTGGAGACGTGCAGGATTAAGATATCGT 898
QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu-AspAlaGluHisTyrLe 320
DB 899 CAGGCCATTACTGCTGTGATCAGGTGATGAGTGTGATGGCTGCTTTGGGACCGGACATATCT 958
QY 320 uGlnGluValGlyValGlnValGlyLysSerAsp 331
DB 959 GCAGGAGTGGGTGCACAGGTGGGCAAGTCTGAT 992

RESULT 2

US-09-540-014-23
; Sequence 23, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioresdoxin and
; TITLE OF INVENTION: NADP-Thioresdoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540.014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-09-540-014-23
Alignment Scores:
Pred. No.: 2,58-178 Length: 995
Score: 1628.00 Matches: 328
Percent Similarity: 98.80% Conservative: 0
Best Local Similarity: 98.80% Mismatches: 3
Query Match: 95.43% Indels: 3
DB: 4 Gaps: 0
US-10-091-841A-9 (1-332) x US-09-540-014-23 (1-995)

QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgValCysIlelleGlySerGlyPro 20
DB 1 ATGAGGGATCCGGCGGCGCGCGCTCCGACGCGGTGTGCATCATCGCAGCGGCCG 60
QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
DB 61 GCCGCGCACAGCGCGCGCATCTACGCGCGCGCGGAGCTCAAGCGCGGTCTTCGAG 120
QY 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
DB 121 GGCTGGATGGCAACGACATCGCGCGCGCGGCGGAGCTCACACCGACCGAGTCTGAG 180
QY 61 AsnPheProGlyPheProThrGlyLeuMetGlyLeuAspLeuMetAspAsnCysArgAla 80
DB 181 AACTTCCCGGATTCCTCCACCGGCATCTGGGATCGACCTCATGGACACTCCCGGCC 240
QY 81 GlnSerValArgPheGlyThrAsnIleLeuSerGluThrValThrGluValAspPheSer 100
DB 241 CAGTCCGTCGCTTCGGCACCAATCTCTCCGAGACCGTCAAGCGGTCTTCGACTTCTCC 300
QY 101 AlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrValVal 120
DB 301 GCCCGCCCTTCGCGGTCACTTCGACTCCACCGCTCTCCGCGACCGTCTCGCGCGTC 360
QY 121 AlaThrGlyAlaValAlaArgLeuHisPheSerGlySerAspThrTyrTrpAsnArg 140
DB 361 GCCACGGCGCGCGCGCGCGCTCCATTTCTCGGTTCGACACCTACTTGGACCGC 420
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
DB 421 GGCATCTCCCGCTCGCGCGCTCGGCGCGCTCGGCCCATCTTCGGACACAGCCCATC 480

QY 161 AlavallieGlyGlyAspSerAlaMetGluGluGlyAenPheLeuThrLysTyrGly 180
Db 481 GCCGTCATCGCGCGGCGGATTCGCCCATGAGAGGCAACTTCCACCAAGTACGGA 540
QY 181 SerGlnValTyrIleIleHisArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 541 TCCCAAGTGATCATCATCCACGGGCGCAACACCTTCGGCGCTCCCAAGATTATGACGGCT 600
QY 201 ArgAlaLeuSerAsnProLysIleGlnValValTyrAspSerGluValValGluAlaTyr 220
Db 601 AGGGCGCTCTCCCAATCTTAAATCCAGGTTCGTGGGACTC-GAGGTCTGAGGCTTAC 659
QY 221 GlyGlyAlaGlyGlyGlyProLeuAlaGlyValLysValLysValLysValLysValLysVal 240
Db 660 GCGGTGACGGGCGGCGGCGGCTTACCTGAGTGGGTCAAGGTCAAGACTTGGTACTGGTGAG 719
QY 241 ValSerAspLeuGlnValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLys 260
Db 720 GTGTCTGACCTTCAGGTCTCGGGCTTTTCTTGGCCATCGGGCATGAGCCGCCACCAAG 779
QY 261 PheLeuAenGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySer 280
Db 780 TTTCATATGGACCTTGAGTCCATGCCGATGGGTATGTGGCCACCAACCGGGCTCT 839
QY 281 ThrHisThrSerValGluGlyValPheAlaGlyAspValGlnAspLysLysTyrArg 300
Db 840 ACACATACAGGTGTGGAGGGTTC-TTGTCTGTGAGACGTCGAGGATAGAGATATCGT 898
QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu-AspAlaGluHisTyrLe 320
Db 899 CAGGCGATTACTGTGTGTGATCAGGTTCATGGGTCTTTGGAGCCGCGAGCACTATCT 958
QY 320 uGlnGluValGlyAlaGlnValGlyLysSerAsp 331
Db 959 GCAGGAGGTGGGTGCACAGGTGGGCAAGTCTGAT 992

RESULT 3

US-09-598-747-26

; Sequence 26, Application US/09598747

; Patent No. 6531648

; GENERAL INFORMATION:

; APPLICANT: Lanahan, Michael B.

; APPLICANT: Desai, Nalini M.

; APPLICANT: Gasdaska, Pamela Y.

; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL

; FILE REFERENCE: A-31383P1

; CURRENT APPLICATION NUMBER: US/09/598,747

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 26

; LENGTH: 1560

; TYPE: DNA

; ORGANISM: Oryza sativa

US-09-598-747-26

Alignment Scores:

Pred. No.: 1,138-159 Length: 1560

Score: 1469.00 Matches: 283

Percent Similarity: 95.47% Conservative: 12

Best Local Similarity: 91.59% Mismatches: 14

Query Match: 86.11% Indels: 0

DB: 4 Gaps: 0

US-10-091-841A-9 (1-332) x US-09-598-747-26 (1-1560)

QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgValCysIleIleGlySerGlyPro 20

Db 406 ATGAGGAGTCCCGCGGCGCGGCTCCGACGCGCTGTGATCATCGGAGCGGCGGCG 465

QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40

:::|||||

Db 466 TCGCGGCACACGGCGGCGGATCTACGCCGCGCGCGGAGCTCAAGCCCGTGTCTTCCAG 525
QY 41 GlyTrpMetAlaAsnAspIleAlaIleGlyGlnLeuThrThrThrThrThrThrThrThrThr 60
Db 526 GCGTGTCTCGCAACGACATCCGCGGCGGCGGCGGAGCTCACACCACCAACCGACGCTCGAG 585
QY 61 AsnPheProGlyPheProThrGlyIleMetGlyIleAspLeuMetAspAsnCysArgAla 80
Db 586 AACTTCCCGGGGTTCGCCGAGGGGATCTTCGCGGCGGAGCTCATGGATCGGTGCGCGCC 645
QY 81 GlnSerValArgPheGlyThrAsnIleLeuSerGluThrValThrValThrValThrValThr 100
Db 646 CAGTCTCTCGGTTCGGCACCATCATCTCCGAGACCGTCCACCGCGGTCCACTTCTCC 705
QY 101 AlaArgProPheArgValThrSerAspSerThrThrValLeuAlaAspThrValValVal 120
Db 706 GCGCGGCGGCTTCGGGTTCGCTCCGACTCCACACCGTCTCGCGGCGGCGGCTCGTCTG 765
QY 121 AlaThrGlyAlaValAlaArgArgLeuHisPheSerGlySerAspThrTyrTrpAsnArg 140
Db 766 GCCACCGGCGGCTCGCGGCGGACTTCCACTTCGCGGCGGCTCCGAGCGCTTACTTGGAA 825
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
Db 826 GGCATCTTCAGCTTCGCCGCTTCGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 885
QY 161 AlaValIleGlyGlyGlyAspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGly 180
Db 886 GCGGTTCATCGCGGCGGCGGACTTCGCGCATGGAGGAGTCCAACTTCTCCACCAAGTAC 945
QY 181 SerGlnValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 946 TCCCATGTGTACATCATCCACCGCGCAACACCTTCGCGGCGGCTCCAAAGTATCATG 1005
QY 201 ArgAlaLeuSerAsnProLysIleGlnValValTyrAspSerGluValValGluAlaTyr 220
Db 1006 AGGCGGTTCGCAACCCCAAGATCCAGGTTTCTCGGAGCTCTCAGGTCTCGGAGGCTAC 1065
QY 221 GlyGlyAlaGlyGlyGlyProLeuAlaGlyValLysValLysValLysValLysValLys 240
Db 1066 GCGCGGCGGAGGTGGAGGTCCATTGGGTGGTCAAGGTGAAGAACTTGGTTACTTGGAA 1125
QY 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 1126 ATCTCCGACCTTCAGGTGTCCGCTCTCTTCTTCGCGCATCGACATGAACCGCGCGAG 1185
QY 261 PheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGlySer 280
Db 1186 TTTCTCGCGCGGCGGAGCTTGAGCTCGATGGGTATGTGGCCACCAACCGGCGGCGTCC 1245
QY 281 ThrHisThrSerValGluGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg 300
Db 1246 AGCACACACGAGTGTGAAGGGGTCTTTGTCTGGGAGTGTGCGAGCAAGAGTATCGC 1305
QY 301 GlnAlaIleThrAlaAlaGlySerGly 309
Db 1306 CAGGCTATTACTGCGGCTGGATCAGGT 1332

RESULT 4

US-09-598-747-24

; Sequence 24, Application US/09598747

; Patent No. 6531648

; GENERAL INFORMATION:

; APPLICANT: Lanahan, Michael B.

; APPLICANT: Desai, Nalini M.

; APPLICANT: Gasdaska, Pamela Y.

; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL

; FILE REFERENCE: A-31383P1

; CURRENT APPLICATION NUMBER: US/09/598,747

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: Patentin Ver. 2.1

```
; SEQ ID NO 24
; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-598-747-24

Alignment Scores:
  Pred. No.:      5,41e-140      Length:      1021
  Score:          1296.00        Matches:      249
  Percent Similarity: 86.77%      Conservative: 33
  Best Local Similarity: 76.62%    Mismatches:   39
  Query Match:      75.97%        Indels:       4
  DB:               4            Gaps:           1

US-10-091-841A-9 (1-332) x US-09-598-747-24 (1-1021)

Qy 11 ThrArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
Db 34 ACCGGCTCTGTCATGTTGGTCTCGGCCCGGCTGCCACACCGCGCATCTACGGCGCC 93
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
Db 94 CGCGCGAGCTCAAGCGGCTCTCTTCGAGGGCTGGATGGCCACGACATCGCCCGCGGC 153
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProThrGlyIleMet 70
Db 154 GGCAGCTCACACACACCGAGCTGTGGAGAACTTCCCGGCTTCCCGAGGGCATCTTC 213
Qy 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
Db 214 GCGCTGGAGCTGACCGACAAAGTTCGCAAGCAGAGCGAGCGCTTCGGCACCACCATCTTC 273
Qy 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
Db 274 ACCGAGCCGTCACAAAGTGAGCTTCTCGAGCAAGCGGCTTCAGCTCTTCCACGAGCTCC 333
Qy 111 ThrThrValLeuAlaAspThrValValValAlaThrGlyAlaValAlaAlaArgArgLeuHis 130
Db 334 AAGGCATCTTCGCGACGCGTGTATCTCGCCATCGCGCGCGTGGCCAAAGTGCTCTCC 393
Qy 131 PheSerGlySerAspThr-----TyrTrpAsnArgGlyIleSerAlaCysAla 146
Db 394 TTCGTGGCTCTCGCGAGTGCTCGGGCGCTCTCGAACCGCGGCATCTCGCGCTGGCT 453
Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 454 GTGTGGCAGCGCGCGCGCCCGATCTTCGCAACAGCGCTCGCTGTGATCGGTGGCGGA 513
Qy 167 AspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGlySerGlnValTyrIleIle 186
Db 514 GACAGCGCATGGAGGAGGCGCAACTTCTCACCAGTACGCTCCAAAGGTGTACATCATC 573
Qy 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuSerAsnPro 206
Db 574 GACCGCGCGAGCGCTTCGCGCTCTCCAGATCATGACGAGCGCGCGCTCTCCACCCG 633
Qy 207 LysIleGlnValValTrpAspSerGluValValGluAlaTyrGlyAlaGlyGlyGly 226
Db 634 AAGATCGACGTCATCTGGAATCTCTCGGTGTGGAGGCTACGCGCAGCGCGAGCGCGAC 693
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnVal 246
Db 694 GTGCTCGCGGCTCAAGGTGAAGAGCTGTGTGACCGGAGCGTGTCTCGACCTCAAGGTG 753
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeu 266
Db 754 TCCGCGCTCTTCTTCGCCATCGGCGACGAGCGCGCCACCAAGTTCCTCGCAGCGCGCGGT 813
Qy 267 GlnLeuHisAlaAspGlyTyrValAlaThrLysProGlySerThrHisThrSerValGlu 286
Db 814 GAGCTGGACTCCGAGCGCTAGTGTGACCAAGCCGGCGCCACCCAGACCTCCGTGCTC 873
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306

; 874 GCGGTGTTTCGCGCGCGCGAGCGTGTGAGGACCAAGTACCGCCGCGCATCACCGCGCC 933
; 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluValGlyAlaGln 326
; 934 GGCACCGGCTGTCATGGCGCGCTCGACCGCCGAGCACTACCTCCAGGAGATCGGTCTCCAG 993
; 327 ValGlyLysSerAsp 331
; 994 CAGGCGCAAGTCCGAC 1008

RESULT 5
US-09-540-014-26
; Sequence 26, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaiz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; PRIOR FILING DATE: 2000-03-31 US 60/127,198
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-540-014-26

Alignment Scores:
  Pred. No.:      1.22e-131      Length:      998
  Score:          1223.50        Matches:      242
  Percent Similarity: 84.62%      Conservative: 33
  Best Local Similarity: 74.46%    Mismatches:   45
  Query Match:      71.72%        Indels:       6
  DB:               4            Gaps:           2

US-10-091-841A-9 (1-332) x US-09-540-014-26 (1-998)

Qy 11 ThrArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
Db 25 ACAAGCTCTGTATCTGATAGGAGTGGCCCGGACACACGGCGCGCATTTACGACGT 84
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
Db 85 AGCGGTGAACCTAAACCTCTCTCTTCGAAAGATGGATGGCTAACGACATCGCTCCCGGT 144
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProThrGlyIleMet 70
Db 145 GGTCAACTCAACCAACACCGCGGT---GAGAAATTTCCCGGATTTCCAGAGGTATTCTC 201
Qy 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
Db 202 GGAGTAGAGCTCACTGACAAATTCGTAACATCGGAGCGATTCGGTACTACGATATT 261
Qy 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
Db 262 ACAGAGACGGTGACAAAGTCGATTCTCTTCGAAACCGTTTAAAGCTATTACAGATTCA 321
Qy 111 ThrThrValLeuAlaAspThrValValValAlaThrGlyAlaValAlaArgArgLeuHis 130
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Db 844 TTGGCGATGAGCAATATATCCGGCATGGGTGTTTCTGTGTGCTACCTGTGATGGA 785
Qy 151 AlalaProilePheArgAsnLysProileAlaValileGlyGlyAspSerAlaMet 170
Db 784 TTT-----TTCTATCGCAAGAAAGATAGCGGTAGTGGCGGAGGTGATCTGCTTC 731
Qy 171 GluGluGlyAsnPheLeuThrLysTyrglySerGlnValTyrllelleHieArgAsn 190
Db 730 GAGGAGGCTCTATCTGGCATCGCTGGCTGAACACGCTGATCTGATCGTACGCAAGAAC 671
Qy 191 ThrPheArgAlaSerLysileMetGlnAlaArgAlaLeuSerAsnProLysileGlnVal 210
Db 670 TATCTCGGTGCTTCAAGTATGACGAGGCGGTGTGATGAATACGCGCAACATACCGTT 611
Qy 211 ValTrpAspSerGluValValGluAlaTyrgly-----GlyAlaGlyGlyProleu 228
Db 610 CTCCTTCGAACATAATACCGGTGGTCTATTTCGCGCAAAACGGTGTGCAAGGTGCTCATCTG 551
Qy 229 AlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnValSerGly 248
Db 550 -----GTGAACGCAAGAGAGCGGACGAGAGAGATGGTGACATGGCCATCGATGTT 497
Qy 249 LeuPhePheAlaileGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeuGluLeu 268
Db 496 TTTTCTCGCTATCGTTCATACGCAACTCGAAGATCTTTCGCGACTACCTCGACTTG 437
Qy 269 HisAlaAspGlyTyValAlaThrLysProGlySerThrHisThrSerValGluGlyVal 288
Db 436 GACGAGTGGTATATCTCGAAGAGTTCCTCCCGCGCAAAAGTTCCCGCGCTA 377
Qy 289 PheAlaAlaGlyAspValGlnAspLysTyArgGlnAlaileThrAlaAlaGlySer 308
Db 376 TTTTGTGCGCGGCGAGTTCGCGACCCACACTATCTGAGGCTATCACGGTTCGCGATCA 317
Qy 309 GlyCysMetAlaAlaLeuAspAlaGluHisTyrlleGlnGluValGly 324
Db 316 GGTTCGAAGCTGCTATCGAAGCAGAGCGTTATTTCGCGAGCAGCGT 269

RESULT 9

US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:

Score:	3,288-68	Length:	4403765
Seq. No.:	723.00	Matches:	159
Percent Similarity:	65.14%	Conservative:	54
Best Local Similarity:	48.62%	Mismatches:	99
Query Match:	42.38%	Indels:	15
DB:	3	Gaps:	6

US-10-091-841A-9 (1-332) x US-09-103-840A-2 (1-4403765)

RESULT 10

US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328

Qy 8 ProLeuArgThrArg-ValCysilelleGlySerGlyProAlaAlaHisThrAlaAla 27
Db 4393993 CCACCCGGTTCGCGACGATGATCGTTCGCTCCGGTCCGCGGGGTACACTCGCGCGCT 4394052
Qy 27 eTyAlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAsp 47
Db 4394053 CTACCGCGCCGCGCCAGCTGGCGCGCTGGTCTTCGAGGGC-----AC 4394097
Qy 47 eAlaAlaGlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProTh 67
Db 4394098 GTCTTTTCGCGCGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4394157
Qy 67 rGlylleMetGlylleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyTh 87
Db 4394158 CGCATCATCCCGGTCGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 4394217
Qy 87 rAsnileLeuSerGluThrValThrGluValAspPheSerAlaArgPropheArg---- 105
Db 4394218 GGACCTGCGTATGGAAGACGTCGAGTCGCTATCATTACCTACCGG---CCGCTGAATCGGT 4394274
Qy 106 -ValThrSerAspSerThrThrValLeuAlaAspThrValValAlaThrGlyAlaVa 125
Db 4394275 CGTCACCGCGCGGACAGACCCACCGCGCGGAGCGGTGATCTGCGCAATGCGCGCAGC 4394334
Qy 125 lAlaArgAlaGlyHisPheSerGlySerAspThrTyTrpAsnArgGlylleSerAlaCy 145
Db 4394335 GGCACGCTATCTCAGGTGCGCGGACAGAGAAATTCGCGCGCGGGGTGAGCTCGT 4394394
Qy 145 sAlaValCysAspGlyAlaAlaProilePheArgAsnLysProileAlaValileGlyG 165
Db 4394395 CGGCACCTGCGCGGATTC-----TTCCTCCGATCAGGACATCGCGTATCGCGCG 4394448
Qy 165 yGlyAspSerAlaMetGluGluGluGluGluGluGluGluGluGluGluGluGluG 185
Db 4394449 CGGTGACTCGCAATGAGAGAGTACTCTCTGACCCGATTCCTGCTGCGAGTGTGACGT 4394508
Qy 185 eileHisArgArgAsnThrPheArgAlaSerLysileMetGlnAlaArgAlaLeuSerAs 205
Db 4394509 GGTGCTATCGCGCGACGAGTTCGCGGCTTCGCAAAATCATGCTCGATCGCGCCGCAACA 4394568
Qy 205 nProLysileGlnValValTrpAspSerGluValValGluAlaTyrglyGlyAlaGlyG 225
Db 4394569 CGACAAGATACGGTTCCTCACCACACACCGGTGCGGTGCGCGGAGACACCC----- 4394623
Qy 225 yGlyProLeuAlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuG 245
Db 4394624 ----ACAGTACCGCGCTTCGCGGTACGCGACACCAACACCGGTGCGCAACACCTGCC 4394679
Qy 245 nValSerGlyLeuPhePheAlaileGlyHisGluProAlaThrLysPheLeuAsnGlyG 265
Db 4394680 GGTAACCGGTGTTTCGTCGCGATCGCGCACGCGCGGTGCGGTGCGGTGCGGTGCGGTGCG 4394739
Qy 265 nLeuGluLeuHisAlaAspGlyTyValAlaThrLysProGlySerThrHisThrSerVa 285
Db 4394740 CATCGAGCTGCGACCGCGCTACGTGTGTCGAGGGCGGTACACACGACCTCCTACT 4394799
Qy 285 lGluGlyValPheAlaAlaGlyAspValGlnAspLysTyArgGlnAlaileThrAl 305
Db 4394800 GCGGCGCGTTCGTCGCGCGACCTGCTGATGATGATGATGATGATGATGATGATGATGATG 4394859
Qy 305 aAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrlleGlnGluValGly 325
Db 4394860 AGCGGCGAGTGGTTCGCGCGCTATCGACCGGAGCGCTGCTGCTGCTGCTGCTGCTGCT 4394916
Qy 325 aGlnValGlyLysSerAsp 331
Db 4394917 AGCAACCGGAGAGCTGAC 4394935

```

; GENERAL INFORMATION:
; APPLICANT: FLRISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 3 29e-68 Length: 4411529
Score: 723.00 Matches: 159
Percent Similarity: 65.14% Conservative: 54
Best Local Similarity: 48.62% Mismatches: 99
Query Match: 42.38% Indels: 15
DB: 6 Gaps: 6

US-10-091-841A-9 (1-332) x US-09-103-840A-1 (1-4411529)

QY 8 ProLeuArgThrArg-ValCysLeileGlySerGlyProAlaAlaHisThrAlaAla1 27
Db 4401757 CCACCCGGTTCGGGAGCTGATGTTATCGCTCCGCGGGGTACACATCGCGCGT 4401816
QY 27 eTyrAlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAsp1 47
Db 4401817 CTACGCCGCCCGTCCAGCTGCGCGCGCTGCTGCTTCGAGGGC-----AC 4401861
QY 47 eAlaAlaGlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProth 67
Db 4401862 GTCTTTTCGGCGGCGCGCTGATGATGATGATGATGATGATGATGATGATGATGATG 4401921
QY 67 rGlyIleMetGlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyTh 87
Db 4401922 CGGCATCACCGTTCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 4401981
QY 87 rAsnIleLeuSerGluThrValThrGluValAspPheSerAlaArgProPheArg----- 105
Db 4401982 GGCACCTGCGTATGGAAGACGTCGAGTCGATGATGATGATGATGATGATGATGATGATG 4402038
QY 106 -ValThrSerAspSerThrThrValLeuAlaAspThrValValAlaThrGlyAlaVa 125
Db 4402039 CGTCACCGCGCGAGCAGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4402098
QY 125 lAlaArgArgLeuHisPheSerGlySerAspThrTyTrpAsnArgGlyIleSerAlaCy 145
Db 4402099 GGCACGCTATCTCAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4402158
QY 145 sAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGly 165
Db 4402159 CGCACCTGCGCGCGGATTC-----TCTTCGCGGATCAGGACGCGCGCGCGCG 4402212
QY 165 YGlyAspSerAlaMetGluGluGlyAsnPheLeuThrLysTyGlySerGlnValTyrl 185
Db 4402213 CGGTGACTCGGCATGAGGAGAGTACCTTCCTGACCGCGCGCGCGCGCGCGCGCG 4402272
QY 185 eIleHisArgArgAsnThrPheArgAlaSerIleMetGlnAlaArgAlaLeuSerAs 205
Db 4402273 GGTGCAATCGCGCGGAGTTCGCGGCTTCCAAATCATGCTCGATCGCGCGCGCGCAAA 4402332
QY 205 nProLysIleGlnValTrpAspSerGluValGluAlaTyGlyAlaGlyGly 225
Db 4402333 CGACAGATACGGTTCCTACCAACCAACCGCGGTGCGGTGCGGAGCGGACACC----- 4402387

; GENERAL INFORMATION:
; APPLICANT: GARY L. BRETTON ET AL.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1552
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1552

Alignment Scores:
Pred. No.: 4 11e-72 Length: 963
Score: 707.50 Matches: 145
Percent Similarity: 63.12% Conservative: 57
Best Local Similarity: 45.31% Mismatches: 101
Query Match: 41.47% Indels: 17
DB: 6 Gaps: 6

US-10-091-841A-9 (1-332) x US-09-328-352-1552 (1-963)

QY 11 ThrArgValCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
Db 31 TCTCGTTAATTAATTCGTTCTGCGCTTCGCGCTTATGTCAGCTGTTATGTCAGCA 90
QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaGly 50
Db 91 CGTCAAAATCTTAAACCAACACACTTATTGTCAGGT-----TTACAGCTTGGC 135
QY 51 GlyGlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProThrGlyIleMet 70
Db 136 GGCCCACTTACACAAACACCGAGTTGACACTGGCGCGCGCGATCTCTGAAGTTTACT 195
QY 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAsnIleLeu 90
Db 196 GGTCTCCCTTAATGAGCGCGTATGCAAGACCATGCTGAACGCTTTTGTACCGAATTGTC 255
QY 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
Db 256 TATGACCATTAATGAGTGGACTTAATGATGCTCTTTTGTCTTAAAGGTGATATG 315
QY 111 ThrThrValLeuAlaAspThrValValAlaThrGlyAlaValAlaArgArgLeuHis 130
```

```
Db 316 GATGAGTACACTGTGATGCTTAAATATTGCAACTGGTGGCAGACGCTCAATATCTTGGC 375
Qy 131 PheSerGlySerAspThrTyrTrpAsnArgGlyIleSerAlaCysAlaValCysAspGly 150
Db 376 TTAGAGTCTGAACAAAATTTATGGGTCAAGCGGTGAGCGCATGTGCAACATGTGATGCG 435
Qy 151 AlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyCysAspSerAlaMet 170
Db 436 TTC-----TTCACAGAACAACAAATGTGATGTTGTTGTTGTTGTTGTTGTTGTTGTT 489
Qy 171 GluGluGlyAsnPheLeuThrLysTyrGlySerGlnValTyrIleIleHisArgArgAsn 190
Db 490 GAAGAAGCACTTTATTATTAATAATATGCTGAACATGTGACATGTGATGACCGCGCGCAT 549
Qy 191 ThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuSerAsnPro-----Lys 207
Db 550 TCTTTACGCTCTGAGAAGATTTTACAAGATCACTTATTGCTAAAGAAAAAGAGCAAA 609
Qy 208 IleGlnValValTrpAspSerGluValValGluAlaTyrGlyAlaGlyGlyPro 227
Db 610 ATCAGTATCGTTTGGAAACCATGAGGTGAAGAGTTCTTGGTGACAATACTGCG----- 663
Qy 228 LeuAlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnValSer 247
Db 664 GTACAGGTGTTGCTTAAATCTACAAAGATGACAGCAACAAAGACAGTCAAGTCAA 723
Qy 248 GlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeuGlu 267
Db 724 GCGTTATTCAATTCGCAATGCGCAATAACCAAAATACCTCTATGTTTGAAGTCAAGTCA 783
Qy 268 LeuHisAlaAspGlyTyrValAlaThrLysProGly-----SerThrHisThr 283
Db 784 TTACGT---GATGCTATATCCAGTACAAAGTGGTACTTTCAGTTAACGCAACAGGACT 840
Qy 284 SerValGluGlyValPheAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIle 303
Db 841 TCTGTACGAGCGCTTTTGTGCTGCTGATGTTGCTGATGTTGCTGATGTTTATGCTCAAG 900
Qy 304 ThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluVal 323
Db 901 ACTTCGGCGGTTTCAGGCTGTATGGCTGCACATAGATGCCGAAATATCTAGATAACCTT 960
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RESULT 12

```
US-09-596-002-28/c
; Sequence 28, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 49617
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte template ID No. 6632636 28
; PUBLIC INFORMATION:
US-09-596-002-28
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Alignment Scores:

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Pred. No.: 1.89e-69 Length: 49617
Score: 707.50 Matches: 141
Percent Similarity: 63.30% Conservative: 66
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Best Local Similarity: 43.12% Mismatches: 103
Query Match: 41.47% Indels: 17
DB: 4 Gaps: 6
```

US-10-091-841A-9 (1-332) x US-09-596-002-28 (1-49617)

```
Qy 4 SerAlaAlaAlaProLeuArgThrArgValCysIleIleGlySerGlyProAlaAlaHis 23
Db 35473 AGTCCCTCTATGTACACAGCACCATCGCTTATCATTTCTTGGCTCAGGCTCCTCAGGATAT 35414
Qy 24 ThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTrpMet 43
Db 35413 TCTCAGCGCTTATGCGCGCGAGCTAATCTAAACCCGCTCATTTATTACAGGC----- 35360
Qy 44 AlaAsnAspIleAlaAlaGlyGlnLeuThrThrThrThrAspValGluAsnPhePro 63
Db 35359 -----TTACAAGTTGGTGGACAGCTAAACACCAACCAACCAAGTTGATACTAGTCCCA 35309
Qy 64 GlyPheProThrGlyIleMetGlyIleAspLeuMetAspAsnCysArgAlaGlnSerVal 83
Db 35308 GGTGATGCACATGTCTGACGGGCAACGGCTTATGAGGAGCAATGAATCCCATGCCGAA 35249
Qy 84 ArgPheGlyThrAsnIleLeuSerGluThrValThrGluValAspPheSerAlaArgPro 103
Db 35248 CGCTTTGGCACCAAGCTTATTATGACAGTATTACCAAGTTGATTACACAATCGCCCT 35189
Qy 104 PheArgValThrSerAspSerThrThrValLeuAlaAspThrValValAlaThrGly 123
Db 35188 TTTACGCTAGTGGCGATAAAGGTGCTTACCTGCGATCCCTTATTATGTGTACAGGT 35129
Qy 124 AlaValAlaArgArgLeuHisPheSerGlySerAspThrTyrTrpAsnArgGlyIleSer 143
Db 35128 GCACCCGACAGTACCTTAGGGCTTGAATCTGAACAAAAGTTTCATGGGTCAAGGTGTTCA 35069
Qy 144 AlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValle 163
Db 35068 GCATGTGCAACTGTGTATGCGCTTT-----TTTTATAAAATCAAAAGTCGTGTTGTC 35015
Qy 164 GlyGlyGlyAspSerAlaMetGluGluGlyAsnPheLeuThrLysTyrGlySerGlnVal 183
Db 35014 GGTGTTGTTAATACCGCTTGTGAAGGCTTATATTATTTATCAATATATCCAGGAGTT 34955
Qy 184 TyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeu 203
Db 34954 ACTTTGATACACCGCGAGATACTTTGCGTGGCCGAAAAAATACTACAAGACCAGTTATTT 34895
Qy 204 SerAsnProLys-----IleGlnValValTrpAspSerGluValValGluAlaTyr 220
Db 34894 GAAAAAGTTAAAGATGTAATATTAAATCGAATGGAAATCATCAATCAAAAGAGTCGTT 34835
Qy 221 GlyGlyAlaGlyGlyProLeuAlaGlyValLysValLysAsnLeuValThrGlyGlu 240
Db 34834 GGTGATGACATGGGC-----GTAACGGGGTTTATGATTGAGTCCACTCAAGATGGCTCA 34781
Qy 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 34780 ATCAACACAGTTAGATATATTATGCGTCTGTTGTTGCCAATGGTCAATAACCAATACCAAG 34721
Qy 261 PheLeuAsnGlyGlnLeuGluLeuHisAlaAspGlyTyrValAlaThrLysProGly--- 279
Db 34720 TTATTTGATGTCATTAATAATATGCAA--GATGATATATCTGTTCAACAGCGGATTA 34664
Qy 280 -----SerThrHisThrSerValGluGlyValPheAlaAlaGlyAspValGlnAsp 296
Db 34663 AACGGCAATGCACAGCAACCAATCAATGGTGTGTTTTTCCGCGTGGTGTGTTGTTGAT 34604
Qy 297 LysLysTyrArgGlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAla 316
Db 34603 CACACCTATCGACAGGCATCACTTCGCGAGGACTGCTGCTGATGCTGCTGCTGCTGCTG 34544
Qy 317 GluHisTyrLeuGlnGluVal 323
Db 34543 GAAAAATATTATGATTCACCTT 34523
```

RESULT 13

US-09-328-352-3988
; Sequence 3988, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3988
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3988

Alignment Scores:

Pred. No.: 5,77e-71 Length: 954
Score: 697.50 Matches: 143
Percent Similarity: 63.44% Conservative: 60
Best Local Similarity: 44.69% Mismatches: 100
Query Match: 40.89% Indels: 17
DB: 4 Gaps: 6

US-10-091-841a-9 (1-332) x US-09-328-352-3988 (1-954)

Qy 11 ThrArgValCysleileGlySerGlyProAlaAlaHisThrAlaAlaIleTyAlaAla 30
Db 16 TCAGCTCTGATAATTCCTCGCTTCTGGCCCTGCGGCTATAGTCAGCAGTATATGCGCG 75
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaGly 50
Db 76 CGTCAAACTTAACCTACTTTAATGCGAGT-----TTACAGCTTGGC 120
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProThrGlyIleMet 70
Db 121 GGCCAACTTACAAACAAACCGAAGTTGACACTGGCGGGCGCATCTGAAGGTTTAAACA 180
Qy 71 GlyIleAspLeuMetAspAsnCysArgAlaGlnSerValArgPheGlyThrAniIleLeu 90
Db 181 GGTCTCTGATTAATGGATCGTATGCAAGACACATGCTGAAGCTTTGGTACAGAACTCTGC 240
Qy 91 SerGluThrValThrGluValAspPheSerAlaArgProPheArgValThrSerAspSer 110
Db 241 TATGACCATATTACGAAGTGGAATTAAGTAGCTCTTCTTCTTAAAGGTGATG 300
Qy 111 ThrThrValLeuAlaAspThrValValValAlaThrGlyAlaValAlaArgArgLeuHis 130
Db 301 GAAGAGTACACATGATGATGCTTTGATTTATGCAACTGGTGTACAGCTCAATATCTTGGC 360
Qy 131 PheSerGlySerAspThrThrTrpAsnArgGlyIleSerAlaCysAlaValCysAspGly 150
Db 361 CTAGAGTCTGAACAAACTTTATGGGACAGCGGTAAAGCATGTGCAACATGTGATGT 420
Qy 151 AlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyAspSerAlaMet 170
Db 421 TTC-----TTCTCAAAAACCAAAAAGTAATGGTTGTAGGTGGTAAACATGCTGTT 474
Qy 171 GluGluGlyAsnPheLeuThrLysTrpGlySerGlnValTyrlleIleHisArgArgAsn 190
Db 475 GAAGAAGCACTTTATTTATCAATATTTGCTTACATGTACGTGTACACCCCGCGAT 534
Qy 191 ThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeu-----SerAsnProLys 207
Db 535 AGCTTACGTTCTGAAAAGATTTTTCAGATCATTTTATTGTCAAAAGAAAAGAACGAAA 594
Qy 208 IleGlnValValTrpAspSerGluValValGlnAlaTyrcGlyAlaGlyGlyPro 227
Db 595 ATCAGCATTTCTGATCAGCAAGTGAAGAGTATTGGGTGACAACTACTGCT----- 648

Qy 228 LeuAlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnValSer 247
Db 649 GTAAACAGTGTTCGCTTAAATCAACTCAAGATGAATCTTAAGCAAGCGTAGAGGTTTCAT 708
Qy 248 GlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGluLeuGlu 267
Db 709 GGTCTATTTCGTTCGAATTTGGCTACAAACCAAAATCTGGTATGTTTGTGGTCAATTAAC 768
Qy 268 LeuHisAlaAspGlyTyTrpValAlaThrLysProGly-----SerThrHisThr 283
Db 769 TTACGT---GATGCTATATCCAAAGTACAAAGCGTACTTCTGCTAATGCAACAGCAACC 825
Qy 284 SerValGluGlyValPheAlaAlaGlyAspValGlnAspLysLysTyArgGluAlaIle 303
Db 826 TCTGTAGCTGGTGTGTTTGGCTGGTGGTACGCTCCTGACAGCATTTATCGCCAAAGCGATT 885
Qy 304 ThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyLeuGlnGluVal 323
Db 886 ACTTCTGCTGATCAGGCTGTATGCTCTAGATGCTGAAAAATATCTAGATCAATTG 945

RESULT 14

US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESS: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/557,884

FILING DATE: 25-Apr-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/476,102

FILING DATE: JUN-5-1995

ATTORNEY/AGENT INFORMATION:

NAME: Michelle S. Marks

REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB186P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1830121 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-557-884-1

Alignment Scores:

Pred. No.: 1.25e-65 Length: 1830121
Score: 695.50 Matches: 150
Percent Similarity: 63.29% Conservative: 50
Best Local Similarity: 47.47% Mismatches: 99
Query Match: 40.77% Indels: 17
DB: 4 Gaps: 6

QY 112 ThrValLeuAlaAspThrValValValAlaThrGlyAlaValAlaArgArgLeuHisPhe 131
Db 1227619 AATTTCACTGTGTGATGCGTATTATTCGCAACAGGTGCTCTGCACGCTATATTGGCTTA 1227560
QY 132 SerGlySerAspThrTyTrpAsnArgGlyIleSerAlaCysAlaValCysAspGlyAla 151
Db 1227559 CTTTCAGAGAAACTACAAAGTCGTGGCGTTCCTGTGTGCAACCTGTGATGGTTTC 1227500
QY 152 AlaProIlePheArgAsnLysProIleAlaValIleGlyGlyAspSerAlaMetGlu 171
Db 1227499 -----TTTATCGTAATAAGCCTGTGTGTGTCATTGGTGAGGAAATACAGCGGTGAA 1227446
QY 172 GluGlyAsnPheLeuThrLysTyGlySerGlnValTyIleIleHisArgAsnThr 191
Db 1227445 GAAGCCCTTTACTTACCCCAATATTCAGTACAGTCAATTTAATCCACCGTCGCGATAGC 1227386
QY 192 PheArgAlaSerLysIleMetGlnAlaArg-----AlaLeuSerAsnProLysIle 208
Db 1227385 TTCCGTGCGGAAATAATCCTTATCGATCGTTTATACAAAAAGTGGAGAGGGAATC 1227326
QY 209 GlnValValTrpAspSerGluValValGluAlaTyGlyAlaGlyGlyProLeu 228
Db 1227325 GTTCTTCATACACTGACCGCACTTTAGATGAAGTATTGGGCGATAATATGGGC-----GTA 1227272
QY 229 AlaGlyValLysValLysAsnLeuValThrGlyGluValSerAspLeuGlnValSerGly 248
Db 1227271 ACTGGATTACGTTAGCCCAACACAAAACTGGGGAGAGAGAACTCAATTAGATGGC 1227212
QY 249 LeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuAsnGlyGlnLeuGluLeu 268
Db 1227211 TTATTCGTGGCGATTGTCATTCGCCAAATACGGAAATTTCCAAAGGGCAACTAGAAATTG 1227152
QY 269 HisAlaAspGlyTyValAlaThrLysProGly-----SerThrHisThrSer 284
Db 1227151 AAT---AATGGCTATATCTGTTGTAATCTGTTCTTGACGGCAATGCACTGCCACTTCT 1227095
QY 285 ValGluGlyValPheAlaAlaGlyAspValGlnAspLysLysTyArgGlnAlaIleThr 304
Db 1227094 GTGGAAGCGGTGTTTCGACAGCGCATGTCTATGATGATCAATATCGCCAGCCATTACC 1227035
QY 305 AlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyIleu 320
Db 1227034 TCCGCAAGAACTGGTTGTATGGCGCCTTGGATGCGAGAACGCTATTATTA 1226987

Search completed: June 21, 2004, 20:53:06

Job time : 3376 secs

QY 601 AGGGGCTCTCAATCCATTAAGATCCAGGTTCTTGGGACTCGAGGTCTCGAGGCTTACG 660
DB 601 AGGGGCTCTCAATCCATTAAGATCCAGGTTCTTGGGACTCGAGGCTTACG 660
QY 661 GGGGTGAGGGGGGGGGCCATTAGTGGGGTCAAGGTCAAGAACTTGGTGAAGTGGTGAAG 720
DB 661 GGGGTGAGGGGGGGGGCCATTAGTGGGGTCAAGGTCAAGAACTTGGTGAAGTGGTGAAG 720
QY 721 TGCTGAAGTTCAGGTCTCGGGCTTTCTTGGCATCGGGCATGAGCCGGCCACCAAGT 780
DB 721 TGCTGAAGTTCAGGTCTCGGGCTTTCTTGGCATCGGGCATGAGCCGGCCACCAAGT 780
QY 781 TTCTCAATGGGAGCTTCAGGTCTCAATCGCATGGTATGTGCGCACCAAGCCGGGCTCTA 840
DB 781 TTCTCAATGGGAGCTTCAGGTCTCAATCGCATGGTATGTGCGCACCAAGCCGGGCTCTA 840
QY 841 CACATACCAGTGTGAGGGGCTTTTGGCTGGAGAGCTGAGGATAGAAAGTATCGTCA 900
DB 841 CACATACCAGTGTGAGGGGCTTTTGGCTGGAGAGCTGAGGATAGAAAGTATCGTCA 900
QY 901 GGCCATTACTGCTGATCAGGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 960
DB 901 GGCCATTACTGCTGATCAGGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 960
QY 961 AGGAGGTGGGTGCACAGGTGGGCAAGTCTGATTGA 995
DB 961 AGGAGGTGGGTGCACAGGTGGGCAAGTCTGATTGA 995

RESULT 3

US-10-425-114-5073
; Sequence 5073, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 5073
; LENGTH: 1286
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700447274_FLI
US-10-425-114-5073

Query Match 74.2%; Score 738.6; DB 13; Length 1286;
Best Local Similarity 85.8%; Pred No. 3.2e-180;
Matches 855; Conservative 0; Mismatches 139; Indels 3; Gaps 3;
QY 1 ATGAGGGATCCGCGCGCGCGCTTCGCGACGCGCGTGTGATCATCGGAGCGGCGCG 60
DB 58 ATGAGGGATCCGCGCGCGCGCTTCGCGACGCGCGTGTGATCATCGGAGCGGCGCG 117
QY 61 GCGGCGCACGCGCGCGCATCTACGCGCGCGCGCGGAGCTCAAGCCGCTCTTCGAG 120
DB 118 GTGCGCACGCGCGCGCATCTACGCGCGCGCGCGGAGCTCAAGCCGCTCTTCGAG 177
QY 121 GGTGATGGGCAACGACATCCGCGGGGGGCGGAGCTCACCACCAACCGAGCTCGAG 180
DB 178 GGTGATGGGCAACGACATCCGCGGGGGGCGGAGCTCACCACCAACCGAGCTCGAG 237
QY 181 AACTTCCCGGATTCGCCACCGGATCATGGGCGATGACCTCATGACAACTGCGCGCC 240
DB 238 AACTTCCCGGATTCGCCACCGGATCATGGGCGGCGGAGCTCATGACAACTGCGCGCG 297

QY 241 CAGTCCGTCCGTTCCGACCAACATCTCTCCGAGACCGTCCACCGAGTCCGACTTCTCC 300
DB 298 CAGTCCGTCCGTTTGGCAACCAATCTCTCCGAGACCGTCCACCGCGCTCGACTTTTCG 357
QY 301 GCGCGCGCTTCGGGTCACTCCGACTCCACACCGTCTCCGCGACACCGTTCGTCGTC 360
DB 358 GCTTCCCATTTCCGAGTTAGTCAAGTCCCAACCGTCTCCGCGATCGGTATCGTT 417
QY 361 GCCACGGGCGCGTCCGCGCGCTTCCATTTCTCCGTTCCGACACCTTATGGAAACCGC 420
DB 418 GCCACGGGAGCGTCCGCGCGCTTCCATTTCCGCGGTCCGATGATGATGATGATGATG 477
QY 421 GGCATCTCCGCTCCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCT 480
DB 478 GGCATCTCCGCTTCCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCT 537
QY 481 GCGGTATCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCC 540
DB 538 GCGGTATCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCC 597
QY 541 TCCCAAGTGTACATCATCCACGGGCGCAACAGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCT 600
DB 598 TCCCAAGTGTACATCATCCACGGGCGCAACAGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCT 657
QY 601 AGGGCGCTCTCCCAATCTTAAGATCCAGGTGTCTGGGACTC-GAGGTCTCTCGAGGCTTAC 659
DB 658 AGGGCGCTTCCCAATCTTAAGATCCAGGTGTCTGGGACTC-GAGGTCTCTCGAGGCTTAC 717
QY 660 GCGGTGAGGGCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCC 719
DB 718 GCGGTGAGGGCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCC 777
QY 720 GTCTCTGACCTTCAGGTCTCCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCC 779
DB 778 GTCTCTGACCTTCAGGTCTCCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCC 837
QY 780 TTTCTCAATGGGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCC 839
DB 838 TTTCTCAATGGGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCC 897
QY 840 ACATACACAGTGTGAGGGG-GTCTTTTGTCTGGGAGAGTGCAGGATAGAGTATCGT 898
DB 898 ACTCACACAGTGTGAGGGG-GTCTTTTGTCTGGGAGAGTGCAGGATAGAGTATCGT 957
QY 899 CAGGCGCATTTACTGCTCTGATCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAG 958
DB 958 CAGGCGCATTTACTGCTCTGATCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAG 1016
QY 959 GCAGGAGGTGGGTGCACAGGTGGGCAAGTCTGATTGA 995
DB 1017 GCAGGAGGTGGGTGCACAGGTGGGCAAGTCTGATTGA 1053

RESULT 4

US-10-425-114-3716
; Sequence 3716, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3716
; LENGTH: 1325

```

; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700336177_FLI
US-10-425-114-3716

Query Match      74.2%; Score 738.6; DB 13; Length 1325;
Best Local Similarity 85.8%; Pred. No. 3.2e-180;
Matches 855; Conservative 0; Mismatches 139; Indels 3; Gaps 3;

QY 1 ATGAGGATCCCGCGCGCGCTCCGACGCGGTGTCATCGGACGCGCGCG 60
DB 87 ATGAGGATCCCGCGCGCGCTCCGACGCGGTGTCATCGGACGCGCGCG 146

QY 61 GCGCGCACACGCGCGCGCTACGCGCGCGCGCGCGCTCAAGCCCGTCTTCGAG 120
DB 147 GCTGCGCACACGCGCGCGCTACGCGCGCGCGCGCGCTCAAGCCCGTCTTCGAG 206

QY 121 GGTGATGCGCAACACATCGCGCGCGCGCGCGCTCACCACACACCGACGTGAG 180
DB 207 GGTGATGCGCAACACATCGCGCGCGCGCGCGCTCACCACACACCGACGTGAG 266

QY 181 AACTTCCCGGATTCGCCACCGCATCGGCGCATCGGCGCTCATGGAACACTGCGCGCC 240
DB 267 AACTTCCCGGATTCGCCACCGCATCGGCGCGCTCATGGAACACTGCGCGCG 326

QY 241 CAGTCGTCGCGTTCGCGACCAACATCTCTCGGACCGGTACCGAGTCACTTCTCC 300
DB 327 CAGTCGTCGCGTTCGCGACCAACATCTCTCGGACCGGTACCGAGTCACTTCTCC 386

QY 301 GCGCGCGCTTCGCGGTCACTCCGACTCACCACCGTCTCGCGACACCGTGTGTC 360
DB 387 GCTTCCCATTCGAGTAGTGAGACTCACAACCGTCTCTCGCGATCGGTTATCGTT 446

QY 361 GCACGCGCGCGTTCGCGCGCGCTCTCAATTTCTCGGTTTCGACACTTCTGGAACCGC 420
DB 447 GCACGCGCGCGTTCGCGCGCGCTCTCAATTTCTCGGTTTCGACACTTCTGGAACCGC 506

QY 421 GGCATCTCCCGTTCGCGGTTCGCGCGCGCTCGCGCTCTCGGACCAAGCCCATC 480
DB 507 GGCATCTCCCGTTCGCGGTTCGCGCGCGCTCGCGCTCTCGGACCAAGCCCATC 566

QY 481 GCGGTCTATCGCGCGCGTGTATTCGCGATGAGAAAGCAACTTCTCAACAGTACGGA 540
DB 567 GCGGTCTATCGCGCGCGTGTATTCGCGATGAGAAAGTCCAAATTTCTCAACAGTACGCGC 626

QY 541 TCCCAAGTGTACATCTACGCGCGCGCAACACTTTCGCGCTTCAAGATTATGCGGCT 600
DB 627 TCCCAAGTGTACATCTACGCGCGCGCAACACTTTCGCGCTTCAAGATTATGCGGCT 686

QY 601 AGGCGCTCTCCAATCTTAAGATCCAGGTTGTCTGGGACTC-GAGGTCTGCGAGGCTTAC 659
DB 687 AGGCGCTCTGAAGACCCCAAAATTAAGTCTCTGGGACTCGGAAGTTGTGAGGCTTAT 746

QY 660 GCGGTCGAGCGCGCGCGCTTACGTGCGGTCAAGTCAAGACTTGTGACTGCTGAG 719
DB 747 GCGGTCGAGCGCGCGCGCTTACGTGCGGTCAAGTCAAGACTTGTGACTGCTGAG 806

QY 720 GTGTCTGACCTTCAGGTGTCTCGGCTTTCTTTCGCGATCGGCGATGAGCGCGCACCAAG 779
DB 807 GTGTCTGACCTTCAGGTGTCTCGGCTTTCTTTCGCGATCGGCGATGAGCGCGCACCAAG 866

QY 780 TTTCTCAATGCGGAGCTTACGTGCGGTTCGCGATGCGGTATGCGCGACCAAGCGCGCTCT 839
DB 867 TTTCTGCGGAGACAGTGTGAATCGATTCAGTGTGATGCGGTATGCGCGACCAAGCGCGCTCT 926

QY 840 ACACATACCACTGTGAGGAGG-GTCTTTGCTGTGAGACGTGAGGATGAAGATATCGT 898
DB 927 ACTCACACCACTGTGAAGGAGGATTTGCTGTGCGACGTGAGGATGAAGATATCGT 986

QY 899 CAGGCCATTACTGTGTGATACGTTGATGCTGCTTTGGGACCGCGACCTATCT 958
DB 987 CAGGCCATTACTGTGTGATACGTTGATGCTGCTTTGGGACCGCGACCTATCT 1045
```

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QY 959 GCAGGAGGTGGTGCACAGGTGGCAAGTCTGATTCA 995
DB 1046 GCAGGAGATCGGTGCACAGGAGGGAAGTCTGATTCA 1082

RESULT 5
US-10-306-292-26
; Sequence 26, Application US/10306292
; Publication No. US20030145347A1
; GENERAL INFORMATION:
; APPLICANT: Lanahan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gaedaska, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; FILE REFERENCE: A-31383PI
; CURRENT APPLICATION NUMBER: US/10/306,292
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US/09/598,747
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-306-292-26
```

```

Query Match      74.1%; Score 737.6; DB 15; Length 1560;
Best Local Similarity 88.6%; Pred. No. 5.9e-180;
Matches 822; Conservative 0; Mismatches 104; Indels 2; Gaps 2;

QY 1 ATGAGGATCCCGCGCGCGCTCCGACGCGGTGTCATCGGACGCGCGCGCG 60
DB 406 ATGAGGATCCCGCGCGCGCTCCGACGCGGTGTCATCGGACGCGCGCGCG 465

QY 61 GCGCGCACACGCGCGCGCTACGCGCGCGCGCGCGCTCAAGCCCGTCTTCGAG 120
DB 466 TCGGCGCACACGCGCGCGCTACGCGCGCGCGCGCGCTCAAGCCCGTCTTCGAG 525

QY 121 GGTGATGCGCAACACATCGCGCGCGCGCGCGCTCACCACACCGAGTTCGAG 180
DB 526 GGTGATGCGCAACACATCGCGCGCGCGCGCGCTCACCACACCGAGTTCGAG 585

QY 181 AACTTCCCGGATTCGCCACCGCATCATGGGCTCATGCGCTCATGGAACACTGCGCGCC 240
DB 586 AACTTCCCGGATTCGCCACCGCATCATGGGCTCATGGAACACTGCGCGCC 645

QY 241 CAGTCGTCGCGTTCGCGACCAACATCTCTCCGACCGTCAAGGAGTTCGATTC 300
DB 646 CAGTCGTCGCGTTCGCGACCAACATCTCTCCGACCGTCAAGGAGTTCGATTC 705

QY 301 GCGCGCGCTTCGCGGTCACTCCGACTCACCACCGTCTCGCGCGACACCGTCTGTC 360
DB 706 GCGCGCGCTTCGCGGTCACTCCGACTCACCACCGTCTCGCGCGACACCGTCTGTC 765

QY 361 GCGCGCGCGGTTCGCGCGCGCTCAATTTCTCGGTTCCGACACTCTGGAACCGC 420
DB 766 GCGCGCGCGGTTCGCGCGCGCTCAATTTCTCGGTTCCGACACTCTGGAACCGC 825

QY 421 GGCATCTCCGCGTTCGCGCGCTCGGCGCTCGGCGCTCTTCCGGAACAAGCCATC 480
DB 826 GGCATCTCCGCGTTCGCGCGCTCGGCGCTCGGCGCTCTTCCGGAACAAGCCATC 885

QY 481 GCGGTCTATCGCGCGGTGATTTCGCCATGAGGAAAGCAACTTCTTCAACAGTACGGA 540
DB 886 GCGGTCTATCGCGCGGTGATTTCGCCATGAGGAGTCCAACTTCTTCAACAGTACGCGC 945

QY 541 TCCGAGTGTATCATCATCCAGCGGCGCAACACTTTCGCGCGCTCAGAGTATTCAGGCT 600
DB 946 TCCGAGTGTATCATCATCCAGCGGCGCAACACTTTCGCGCGCTCAGAGTATTCAGGCT 1005
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Qy	601	AGGCGCTCTCCAAATCTTAAGATCCAGGTTGTCTGGGACTC-GAGGTCTGCGAGGCTTAC	659
Db	1006	AGGCGGTGTCAAAACCCCAAGATCCAGGTTTTCTGGGACTCTGAGGTCTGCGAGGCTTAC	1065
Qy	660	GGGGGTGCAGCGCGCGGCCCAATTAGCTGGGGTCAAGGTCAAGAATCTGGTGACTGGTGAG	719
Db	1066	GGCGGCGAGGTTGGAGGTCATTGGCTGGTGTCAAGGTGAAGAACTTGGTTACTGGGAAG	1125
Qy	720	GTGTCTGACCTTCAGGTGTCCGGGCTTTTCTTCCCATCGGGCATGAGCCGGGCCACCAAG	779
Db	1126	ATCTCCGACCTTCAGGTGTCCGGTCTCTTTTGGCCATCGGAATGAACCGGCGGACGAAG	1185
Qy	780	TTTCTCAATTGGGCGAGCTTGAGCTTCATCGGATGGGTATGTGGCCACCAAGCCGGGCTCT	839
Db	1186	TTTCTCGCGGGCAGCTTGAGCTCGATGCTGATGGGTATGTGGCCACCAAGCCAGGCTCC	1245
Qy	840	ACACATACCAGTGTGGA-GGGGCTTTGCTGCTCGGAGACGTCGAGNTAGAAGTATCGT	898
Db	1246	ACGCACACCAAGTGTGAAGGGGGTCTTTTGTCTGGGGATGTGCAGGACAAGAAGTATCGC	1305
Qy	899	CAGGCCATTACTGCTGCTGGATCAGGTT	926
Db	1306	CAGGCTATTACTGCGCTGGATCAGGTT	1333

RESULT 6

```

US-10-306-292-24
; Sequence 24, Application US/10306292
; Publication No. US20030145347A1
; GENERAL INFORMATION:
; APPLICANT: Lanahan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gasdaska, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; THEREIN
; FILE REFERENCE: A-31383P1
; CURRENT APPLICATION NUMBER: US/10/306,292
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US/09/598,747
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-306-292-24

```

Query Match	55.4%	Score	551.6	DB	15	Length	1021
Best local Similarity	75.0%	Pred. No.	3.8e-132				
Matches	747	Conservative	0	Mismatches	234	Indels	15
Gaps	4						
QY	12	CGCGCGCGCGCGCTTCGCGACGCGCGGTGTGCATCATCGCGAGCGCGGCCGCGCGCGACAC	71				
Db	15	CGGCGTGGAGACTACAACACCCGCCCTCTGCATCGTGTGGCTCCGGCCCGACTGCCACAC	74				
QY	72	GGGGGCATCTACGCGCGCGCGCGGAGCTCAAGCCCGTCTCTTCGAGGGCTGGATGGC	131				
Db	75	CGCGCGCATCTACGCGCGCGCGCGGAGCTGAAGCCGCTCCTCTTCGAGGGCTGGATGGC	134				
QY	132	CAACGACATCGCGCGCGGGGGCCAGCTTCACCCACCACCGACGTCGAGAACTTCCCGCG	191				
Db	135	CAACGACATCGCGCGCGGGGCCAGCTTCACCCACCACCGACGTCGAGAACTTCCCGCG	194				
QY	192	ATTCCCCACCGGATCATGGCATTCGACCTCATGGAACAATCGCGCGCCAGTCCGTCG	251				
Db	195	CTTCCCGGAGGGATCTCTGGCTGGAGCTGACCGACAGTTCCGCAAGCAGAGCAGCG	254				
QY	252	CTTCGGACCAACATTCCTTCGAGACCGTGACCGAGGTGCAATTCTCCGCCCGCCCTT	311				
Db	255	CTTCGGACCAACCATCTTTCACCGAGACCGTGACCAAGGTGCAATTCTTCGAGCAAGCGTT	314				
QY	312	CCGCGTCACCTTCGACTCCACCAACCGTCTTCGCGGCACACCGTCTGTCGTCCACACGGGCGC	371				

[illegible]

RESULT 7

```

US-10-425-114-29681
; Sequence 29681, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Xongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 29681
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-GMFLMINSOY117H06_FLI
US-10-425-114-29681

```

Query Match	53.2%	Score 529	DB 13	Length 1284
Best Local Similarity	75.1%	Prod. No. 2.5e-126		
Matches 732	Conservative 0	Mismatches 225	Indels 18	Gaps 5
Qy	38	TGTGCATCATGGCAGCGCCGCGCGCACGACGGGGCCATCTACGGCGCGCGCGCGG	97	
Db	64	TCTGCATCATCGGAAGCGTCCCTCCGCGCCACACAGCGCGGTCTACGCGCTCGAGCGG	123	
Qy	98	AGCTCAAGCCCGTGCTCTTCAGAGGCTGGATGGCCAAAGCATCGCCGCGGGGGCGCAGC	157	
Db	124	AGCTGAAGCCGATCCTCTTCAGAGGCTGGATGGCCAAAGCATCGCCCGCGGGCGCGCAGC	183	
Qy	158	TCACCAACCAACCCAGCGTGGAGAACTTCCCGGATTCGCCACCGGCATCATGGGCATCG	217	
Db	184	TCACCAACCAACCGACGTCGAGAACTTCCCGGTTCCCGACGGCATCTCTGGCGCGG	243	
Qy	218	ACCTCATGACAACTCGCGCGCCCGACGTCGCTTCGGTTCGGACACAAATCCTCTCCGAGA	277	
Db	244	AGCTCATGGAACGTCGCGGAGCCAGTCGCTTCGCTTCGGCACCGAGATCAACACCGAGA	303	
Qy	278	CCGTCACCGAGGTGCACTTCTCCGCCCGCCCTTCGCGTCACCTCCGACTTCCACCAACCG	337	
Db	304	CCGTCCTCAAGTCGATTTCTCGAACCGTCTCTTCAGGGTTTTACCGATTCGCCGAACCG	363	
Qy	338	TCCTCGCGGACACCGTCGTCGCGCACGGGCGCGTCGCGCGCGCGCTCATTTCTCCG	397	
Db	364	TGAGGCCGAATCCGTCATGTCGCGCACCGGTGCGCTCGCCCAAGCGCTTCCCTTCCCGG	423	
Qy	398	GT-----CCGACACCTACTGGAACCGCGCATCTCCGCTCGCGCGCTCTGCG	445	
Db	424	GCTCCGCGGACGCGCCCGAAGGCTACTTGAACCGTGAATCTCCGCTGCGCGCTCTGCG	483	
Qy	446	ACGCGCTCGGCCCATCTTCGGGAACAGCCCATCGCGCTCATCGCGGGGGTGATTCG	505	
Db	484	ACGCGCGCGCCCGATCTTCGGGAACAGCCGCTGCGAGTGATCGCGCGGGAGACTCCG	543	
Qy	506	CCATGGAAGGCAACTTCTCCACCAAGTACCGATCCCAAGTGATCATCATCCACGGC	565	
Db	544	CCATGGAAGGACCACTTCTCCACCAAGTACCGTTCGGAAGTTTACATATTCACCGTA	603	
Qy	566	GCACACTTCCGCGCTCCAGATTTGCGGCTAGGGGCTCTCCAACTCTAAGATCC	625	
Db	604	GGGATCGTTCAGGGCTTCGAAGATTTGCGAGCAAGGTGATGAATATAGTAAAGTAA	663	
Qy	626	AGGTGTCTGGGACTC-GAGGTCTGAGGCTTACCGCGGTGACGGGGCGGGCCCATAG	684	
Db	664	AGGTGATTTGGAATTCGGTGTGCTGAGGCTTTTGGGGCGGAGATAACAAGAGGTGC	723	
Qy	685	CTGGG---TCAGGTCAAGAACTTGCTGACTGTGTGAGGTGTCTGACCTTCAGGTGTCG	741	
Db	724	TTGGGGGATGAAGGTGAAGAAATGTGTGACTCAAGAGGTGTCTGAATGAAGGTTCGT	783	
Qy	742	GGCTTTTCTTCGCCATCGGGGCACTAGCGCGGCACCAAGTTTCTCAATGGGCGAGCTTGAGC	801	
Db	784	GGTTGTTTTTCGCAATTTGGGCACGAGCCCGACCAAGTTCTTGAGCGGGCAGCTTGAAT	843	
Qy	802	TCCATGCGGATGGTATGTGGCCACCAAGCGGGCTCTACACATACAGGTGGAGGG-G	860	
Db	844	TGGATCTGATGGATATATTGTGACGAAGCCGGGACGAGCAACCAAGTGTGGAGGGAG	903	
Qy	861	TCCTTGTCTGGAGACGTGCAGGATGAAGATTCGTCAAGCCCAATTTACTGCTGCTCGAT	920	
Db	904	TGTTTGTCTGGGATGTTTCAGGACAAAGTATAGCAAGCTATTACTGCTGCTGCA	963	
Qy	921	CAGGTCGATGCGCTTTTGGGACCGCGACACTATCTGAGGAGGTGGGTGACACAGTG	980	
Db	964	CTGATGCAATGGCTGCTTTT-GGATGCGAAGCAATTACCTTCGAAAAATGTGGTTTACAA	1022	
Qy	981	GGCAAGTCTGATTGA	995	
Db	1023	GATAAGAGTGATTGA	1037	

```

RESULT 8
US-10-424-599-65583
  / Sequence 65583, Application US/10424599
  / Publication No. US20040031072A1
  / GENERAL INFORMATION:
  / APPLICANT: La Rosa Thomas J
  / APPLICANT: Kovalic David K
  / APPLICANT: Zhou Yihua
  / APPLICANT: Cao Yongwei
  / TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
  / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
  / FILE REFERENCE: 38-21(63223)B
  / CURRENT APPLICATION NUMBER: US/10/424,599
  / CURRENT FILING DATE: 2003-04-28
  / NUMBER OF SEQ ID NOS: 285684
  / SEQ ID NO 65583
  / LENGTH: 1645
  / TYPE: DNA
  / ORGANISM: Glycine max
  / FEATURE:
  / OTHER INFORMATION: Clone ID: PAT_MRT3847_30236C.1
US-10-424-599-65583

```

Query Match	52.7%	Score 524.2	DB 13	Length 1645
Best Local Similarity	74.8%	Pred. No. 4,4e-125		
Matches 729	Conservative 0	Mismatches 228	Indels 18	Gaps 5
QY	38	TGTGATCATCGGACGGCCCGCGCACACGGCGGCATCTACGGCGCCCGCGCGG 97		
Db	176	TCTGATCATTGGAAAGCGGTCCCTCCGCCACACAGCGCGCTTACGCGCTCGAGCGC 235		
QY	98	AGCTCAAGCCCGTGCTCTTTGAGGGCTGGATGSCCAACGACATCGCCGCGGGGGCCACG 157		
Db	236	AGCTGAAGCCGATCTCTTTCGAGGGCTGGATGGCCAAACGACATCGGCCCGCGCGCCAGC 295		
QY	158	TCACACACACACCGAGCTCGAGAACTTCCCGGATTCGCCACCGCGCATCTAGGGCATCG 217		
Db	296	TCCACACACACCGAGCTCGAGAACTTCCCGGGTTCCCGACGGCATCTCGGGCGGG 355		
QY	218	ACCTCATGGACAACTGGCGCGCCAGTCGGCTTCGGCACCAACATCTCTCCGAGA 277		
Db	356	AGCTCATGGAAGCTGCGGAGCCAGTCGCTCCGCTTCGGCACCGAGATCCACACGAGA 415		
QY	278	CGGTACACGAGGTGCACTTCTCGCGCCGCCCTTTCGCGCTGCATCTCGACTCCACACCG 337		
Db	416	CGGTCTTCAAAGTCGATTTCTCGAACCGCTCTTTCAGGGGTTTTTCACCGATTCGGAACCG 475		
QY	338	TCTCGCGCGACACCGTGTGTGTGTCGCACGGCGCGCTTCGGCGCGCGCTCCATTTCTCG 397		
Db	476	TCGAGCGCGAATCTCGTCATCGTCCGCACCGCGCGCTTCGCCAAGCGCTTCCCTTCCCG 535		
QY	398	GTT-----CCGACACTTACTGGAACCGCGCATCTCCGCTTCGCCGCTGTGCG 445		
Db	536	GCTCGCGGATGGCCCGATGGCTACTTGGAAACCGCGCATCTCCGCGTCGCGCTGTGCG 595		
QY	446	ACGGCGCTGCGCCCATCTTTCGGNACAAAGCCCATCGCGCTCATCGCGGGGGTGATTCCG 505		
Db	596	ATGGCGCGCGCCCATCTTTCGGAAACAAAGCCCATTCGGCGGTGATTCGGCGCGGGGACTCG 655		
QY	506	CCATGGAGGAAGGCAACTTCTCTACCAAGTACGGATCCCAAGTGATCATCTCCACCGGC 565		
Db	656	CGATGGAGGAGCCACCTTCTTCTCACCAGTACGGTTCCGAGGTTTACATAATTCACCGCA 715		
QY	566	GCACACACTTTCGGCGCTCCAAAGATATGACGGCTTAGGGCGTCTCCAAATCTATAGATCC 625		
Db	716	GGGATACATTCAGGGCTTCGAAGATATGACAGACGAAGTTATGGGCAATAGCAAGATTA 775		
QY	626	AGGTTGCTGGGATC-GAGTCTGTGAGGCTTACGGCGGTGACGGCGCGCGCCCATTAG 684		
Db	776	AGGTGATTTGAAATTCGGTGGTGGTTCGAGGCTTTGGGGCGGAGNATACAGAGGGTGC 835		
QY	685	CTGGGG---TCAAGTCAAGAACTTGGTGACTCGTGAGGTGTCTGACCTTCAGGTGTCCG 741		

Db 836 TTGGGGGATTAAGGTGAAGAAATGTTGCTGACTCGAGAGTATCTGAAATTAAGGTTTCTG 895
Qy 742 GGCTTTTCTTCGGCCATCGGCATGAGCCGCCACCAAGTTTCTCAATGGCGAGCTTGAGC 801
Db 896 GGTGTTTCTTCGCAATTTGGGACAGCCCGGACCAAGTTCTTGGACGGGAGCTTGAAT 955
Qy 802 TCCATGCCGATGGGTATGGCCACCAAGCCGGCTCTACACATACAGTGTGGAGG-G 860
Db 956 TGAATTTCTGATGATATATTGTACGAAGCCGGGACGACGAGACCACTGTTGAGGGAG 1015
Qy 861 TCTTTGCTGCTGAGAGCTGACGATAAGAGTATCGTCAAGGCCATTACTGCTGCTGGAT 920
Db 1016 TGTGTTGCTGCTGGGATGTTTCAGACCAAGAGTATAGGCAAGTATTACTGCTGCTGCA 1075
Qy 921 CAGGTTGATGCTGCTTTGGGACCGGACCACTATCTGACGAGGTGGGTGCACAGGTG 980
Db 1076 CTGGATGATGCTGCTGCTTT-GGATGACAGACATTACTGCAAAATGTTGTTTACACAA 1134
Qy 981 GGCAAGTCTGATTGA 995
Db 1135 GATAAGAGTGTATTGA 1149

RESULT 9
US-10-424-599-13171
; Sequence 13171, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 13171
; LENGTH: 964
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_1118C.1
US-10-424-599-13171

Query Match 47.9%; Score 476.8; DB 13; Length 964;
Best Local Similarity 71.6%; Pred. No. 6.6e-113;
Matches 686; Conservative 0; Mismatches 257; Indels 15; Gaps 4;

Qy 28 CGCACGCGGTGTGATCATCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 87
Db 7 CGTCCGAAGCTCTGATCATCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 66
Qy 88 GCCGCGCGGAGCTCAAGCCGCTCTTTCGAGGCTGATGCGGCGGCGGCGGCGGCGGCGGCGG 147
Db 67 CGCGCGCGGAGTTGAAGCGGCTCTTTCGAGGCTGATGCGGCGGCGGCGGCGGCGGCGGCGG 126
Qy 148 GGGGGCCAGCTCACCAACACCGAGCTCGAGAACTTCCCGGATTCGCCAGTCCCGGCGGCGG 207
Db 127 GGTGGCCAGCTCACCAACACCGAGCTCGAGAACTTCCCGGATTCGCCAGTCCCGGCGGCGG 186
Qy 208 ATGGGATGACCTCATGGAACACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 267
Db 187 CTCGGACCGGAGTTCATGAGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 246
Qy 268 CTCTCCGAGACCGTCAACCGAGGTCGATCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 327
Db 247 GTACGAGGACCGTCAACCGAGGTCGATCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 306
Qy 328 TCACACGACCGTCTCGGCGGACACCGTGTGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 387
Db 307 TCCACCGACCGTGGAGGCGGAGTCCGTGTGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 366

RESULT 10

US-10-290-072-38
; Sequence 38, Application US/10290072
; Publication No. US20030211511A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Daimia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Lugimbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-3
; CURRENT APPLICATION NUMBER: US/10/290,072
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/376,682
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 6357
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-290-072-38

RESULT 11

US-10-141-531-38

Sequence 38, Application US/10141531

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LENGTH: 6357

TYPE: DNA

ORGANISM: Arabidopsis thaliana

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Query Match 43.0%; Score 427.4; DB 15; Length 6357;

Best Local Similarity 67.5%; Pred. No. 3.9e-100;

Matches 666; Conservative 0; Mismatches 306; Indels 15; Gaps 4;

QY 23 CGTCCGCGACGCGGTGTCATCATCGGACGGCGCGCGCGGACACGACGGCGGCATCT 82

DB 5350 CTCACAAACAAGGCTCTGTATCGTAGGAAGTGGCCCGGACACACGCGCGCGCATTT 5409

QY 83 ACGCGGCGCGCGGGAGCTCAAGCCCGTGTCTTCGAGGGCTGGATGGCCACGACATCG 142

DB 5410 ACGCAGTAGGGCTGAACTTAAACCTTCTCTTCGAAGATGGATGGCTAACGACATCG 5469

QY 143 CCGCGGGGCGAGCTCCACACACACGAGTGCAGAACTTCCCGGATTCGCCACCG 202

DB 5470 CTCGCGTGTCAACTAAACAACACACGACGCTCGAAGTTTCCCGGATTTCCAGAAG 5529

QY 203 GCATCATGGCATCGACCTCATGAGCAACTGCGCGCGCCGACGTCGTCGCTTCGGCACCA 262

DB 5530 GTATTCTCGAGTAGAGTCACTGACAAATTCGTAAACAATCGGACGATTCCGTACTA 5589

QY 263 ACATCTCTCGAGACGGTCACGAGTGCAGTCTTCGCGCGCCCTTCGCGTCACT 322

DB 5590 CGATATTTACAGAGACGGTCAGAAAGTCATTTCTTCGAAACCGTTTAAGCTATTCA 5649

QY 323 CCGACTCCACACCGCTCTCGCGACACCGTCGTCGTCGCGACGGCGCGCTCGCGCGCC 382

DB 5650 CAGATTCGAAGGCCATTCTCGTACGCTGTGATTCTCGTACTCGAGCTGTGGCTAAGC 5709

QY 383 GCCTCCATTTC-----TCCGGTTCGACACCTACTGGACCGCGGATCTCCG 430

DB 5710 GGCTTAGTCTCGTTGGATCTGGTGAAGGTTCTGGAGGTTCTTGGAAACCGTGGAAATCTCCG 5769

QY 431 CCTGCGCGCTCTCGACGGCGCTCGCCCCATCTTCGCGAACCAAGCCCATCGCGCGTCATCG 490

DB 5770 CATGCGCTGTTTCGACGGAGCTGCTCCGATATTCGTAAACAACTCTTTCGCGTATCG 5829

QY 491 CGCGCGTGTATTCGCCATGGAGAGGCACTTCTCTCCACAGTAGCGATCCCAAGTGT 550

DB 5830 GTGAGCGCATTCAGCAATGGAAGAGCAAACTTTCTTCAAAATATGATCAAAAGTGT 5889

QY 551 ACATCATCCACGGGCGCAACCTTCGCGCGCTCCCAAGATTATGAGGCTAGGCGCTCT 610

DB 5890 ATATAATCCATCGCGGATGCTTTTCGTGCTTAAGATTATGACAGACGCGCTTGT 5949

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Qy 969 GGTGCACAGGTGGGCAAGTCTGATTGA 995

Db 6309 GGATCTCAGCAAGGTAAAGAGTATTGA 6335

Search completed: June 21, 2004, 19:56:43
Job time : 496 secs